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8-510

198134

mg

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From: Jiang, Dong
Sent: Wednesday, August 09, 2006 5:52 PM
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Subject: 10/719,202

ETD = 716100

Please search residues 197-2218 of SEQ ID NO:1, and 2.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

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REM - 4D70
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: August 16, 2006, 21:10:44 ; Search time 2561 Seconds
(without alignments)
9701.522 Million cell updates/sec
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Perfect score: 2022
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 18982170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1962.2	97.0	2287	16	US-11-150-533-29
5	1940	95.9	2328	3	US-09-899-471-4
6	1940	95.9	2328	8	US-10-719-202-4
7	1933.6	95.6	2128	3	US-09-866-050A-487
8	1933.6	95.6	2128	6	US-10-152-661-487
9	1933.6	95.6	2314	3	US-09-863-818A-7
10	1933.6	95.6	2314	9	US-10-749-144-7
11	1933.6	95.6	2314	9	US-10-924-667-7
12	1929.6	95.4	2331	8	US-10-416-442A-74
13	1412.2	69.8	2022	3	US-09-899-471-3
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19	1113.4	55.1	2380	3	US-09-874-503-13	Sequence 13, Appli
20	1113.4	55.1	2380	3	US-09-747-259-13	Sequence 13, Appli
21	1113.4	55.1	2380	3	US-09-908-827-13	Sequence 13, Appli
22	1113.4	55.1	2380	6	US-10-006-867-161	Sequence 161, App
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ALIGNMENTS

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; Sequence 1, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(2218)
US-09-899-471-1

Query Match					100.0%;	Score 2022;	DB 3;	Length 2256;
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Qy	1	ATGCGCTGTCTCTGTTCTCTGCTGCTCTGCGACCTGGCGGAAACCTGTGTCTCTCT	60					
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Qy	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTCTCTAGGCTCTCTCTGCCCAC	120					
Db	257	CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTCTCTAGGCTCTCTCTGCCCAC	316					
Qy	121	CTCTGGATGTGACGTGCTCTGCTGCTGCTGGAAGCTTCAGTCTGCCCCAGGCTGTG	180					
Db	317	CTCTGGATGTGACGTGCTCTGCTGCTGCTGGAAGCTTCAGTCTGCCCCAGGCTGTG	376					
Qy	181	CTAGTGTCTTACCCGCTTCAGAGCGAGCTGGTGCTGAGTGTCACAGAGACAGATTGC	240					
Db	377	CTAGTGTCTTACCCGCTTCAGAGCGAGCTGGTGCTGAGTGTCACAGAGACAGATTGC	436					

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Db |||||
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Qy |||||
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Db |||||
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; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(2218)
US-10-719-202-1

Query Match 100.0%; Score 2022; DB 8; Length 2256;

Thu Aug 17 14:34:40 2006

APPLICANT: Burkhead, Steven K.
APPLICANT: Levin, Steven D.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
APPLICANT: Jaspers, Stephen R.
APPLICANT: Bilborough, Janine
TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 04-06P1
CURRENT APPLICATION NUMBER: US/11/150,533
CURRENT FILING DATE: 2005-06-10
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 2269
TYPE: DNA
ORGANISM: Mus musculus
US-11-150-533-25

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DB 257 CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTGCTCTTAGGCCCTCTCCTGCCAC 316
QY 121 CTCTGGCATGTGACGCTGCTCTGCTGCTTGGAGCCTCCAGCTCTGCCCGAGCCCTGTG 180
DB 317 CTCTGGCATGTGACGCTGCTCTGCTGCTTGGAGCCTCCAGCTCTGCCCGAGCCCTGTG 376
QY 181 CTAGTGGCTACCCGCTGCGAGACGGAGCTGGTCTGAGGTGTCCACAGAGACAGATTGC 240
DB 377 CTAGTGGCTACCCGCTGCGAGACGGAGCTGGTCTGAGGTGTCCACAGAGACAGATTGC 436
QY 241 GCCCTCGGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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QY 361 GTGGTGTCTCTCTTCCAGGCTTACCCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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DB 617 CCCGCTGACCTGGTGCAGCCTGGTCCAGTCCGTGGGTTCCTGGGTATTTGACTGTTTCGAG 676
QY 481 GCTAGTCTTGGGCTGAGGTACAGTCTGCTTACAGAGCCAGGTACAGAAAGAG 540
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DB 1937 TGGGTGTACTCCGATTTCTTGCAGGCGCGGCGCGCATGAGCCCTCGCCCTCTGGCTCAGC 1996
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Db 2177 TGTACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGGAATGGGACCTTGGGACCTTGCACCT 2236
Qy 2014 AACTAGAA 2022
Db 2237 AACTAGAA 2245

RESULT 4
US-11-150-533-29
; Sequence 29, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; FILE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-150-533-29

Query Match 97.0%; Score 1962.2; DB 16; Length 2287;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 3; Indels 45; Gaps 1;

Qy 1 ATGCTGTGTCTGTGTTCTGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 197 ATGCTGTGTCTGTGTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
Qy 61 CTGGAGAGACTGATGAGGCTCAGGACACTGACGCTGCTCTAGGCTCTCTAGGCTCTCTAGGCT 120
Db 257 CTGGAGAGACTGATGAGGCTCAGGACACTGACGCTGCTCTAGGCTCTCTAGGCTCTCTAGG 316
Qy 121 CTCTGGAGTGTGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 317 CTCTGGAGTGTGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
Qy 181 CTAGTGCCTACCGCTCTGACGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 377 CTAGTGCCTACCGCTCTGACGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
Qy 241 GCGCTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 437 GCGCTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
Qy 301 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAAAGGCTCTCTCCAGGCGCCAG 360
Db 497 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAAAGGCTCTCTCCAGGCGCCAG 556

Qy 361 GTGGTGTCTCTCTTCCAGGCTTACCCCAATCGCCCGCTGTGTGCCCTGTGTGAGGTCCAGGTG 420
Db 557 GTGGTGTCTCTCTTCCAGGCTTACCCCAATCGCCCGCTGTGTGCCCTGTGTGAGGTCCAGGTG 616
Qy 421 CCGCTGTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 617 CCGCTGTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
Qy 481 GCTAGTCTTGGGGCTGAGGTACAGATCTGCTGCTTACACGAAAGCCAGGTACACGAAAGAG 540
Db 677 GCTAGTCTTGGGGCTGAGGTACAGATCTGCTGCTTACACGAAAGCCAGGTACACGAAAGAG 736
Qy 541 CTCACCTTACACAGGAGCTGCTT----- 564
Db 737 CTCACCTTACACAGGAGCTGCTTGAAGTCCGGGACAGCATCCAG 796
Qy 565 -----GATGGTGACAAATGCTCTTCTGACACTGGATGCTCTGAGGAGCAGGACTTT 615
Db 797 AGCTGTGGGATGGTGACAAATGCTCTTCTGACACTGGATGCTCTGAGGAGCAGGACTTT 856
Qy 616 AGCTTCTTACTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Db 857 AGCTTCTTACTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
Qy 676 CTGACTGAGCTTACAGAACTTACTTTAAACACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTG 735
Db 917 CTGACTGAGCTTACAGAACTTACTTTAAACACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTG 976
Qy 736 CAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
Db 977 CAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1036
Qy 796 CCGGTGTGACACAGGAACTCTGGACATAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
Db 1037 CCGGTGTGACACAGGAACTCTGGACATAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
Qy 856 TGGCAGCTAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
Db 1097 TGGCAGCTAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
Qy 916 GACCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975
Db 1157 GACCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216
Qy 976 GAGCCACAGATTTCCAGTTGGTGGCAGGCCACCCCAACCTCTGCTGCTGCTGCTGCTGCTGCTG 1035
Db 1217 GAGCCACAGATTTCCAGTTGGTGGCAGGCCACCCCAACCTCTGCTGCTGCTGCTGCTGCTGCTG 1276
Qy 1036 TGGGAGAGGTTTACAGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
Db 1277 TGGGAGAGGTTTACAGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1336
Qy 1096 GATATGCTTGTAGTGGAGATGAACCGGCTTCAACAAACATCATGCTGCTGCTGCTGCTGCTG 1155
Db 1337 GATATGCTTGTAGTGGAGATGAACCGGCTTCAACAAACATCATGCTGCTGCTGCTGCTGCTG 1396
Qy 1156 CCGCTGCTGTGTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1215
Db 1397 CCGCTGCTGTGTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
Qy 1216 GAGTTGTGTGACAGCTTCCGATCACACAGTGTATGAGCTGTGGAACGATGACACATG 1275
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Db 1517 GATGCTGTATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576
Qy 1336 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1395
Db 1577 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1636
Qy 1396 AGGAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1455

[illegible]

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Db	481	GCTAGTCTTTGGGGCTGAGGTA	CAGATCTGTGTCCTACAGAAAGCCAGGTAACGAAAGAG	540
Qy	541	CTCAACCTTCACACAGCAGCTGCCT	-----	564
Db	541	CTCAACCTTCACACAGCAGCTGCCT	GACTGCAAGGGGTCTTGAGTCCGGGACAGCATCCAG	600
Qy	565	-----	-----GATGGTGACAATGCTCTTCTGACA	588
Db	601	AGCTGCTGGGTCTGCCCCCTG	GCTCAATGTGTCTACAGATGGTGACAATGCTCTTCTGACA	660
Qy	589	CTGATGTCTCTGAGGACGAGGA	CTTTAGCTTTTATCTGTACTGTGCGTCCAGTCCCGGAT	648
Db	661	CTGATGTCTCTGAGGACGAGGA	CTTTAGCTTTTATCTGTACTGTGCGTCCAGTCCCGGAT	720
Qy	649	GCTCTCAAACTCTGTGGTCAAAA	CCCTGACTGGACCTCAGAACCTCAGAACATTACTTTAAACCAC	708
Db	721	GCTCTCAAACTCTGTGGTCAAAA	CCCTGACTGGACCTCAGAACATTACTTTAAACCAC	780
Qy	709	ACAGACCTGGTTCCTGCTCTG	CAATTCAGGTGTGGTCTGTAGAGCCAGACTCTGTAGAGG	768
Db	781	ACAGACCTGGTTCCTGCTCTG	CAATTCAGGTGTGGTCTGTAGAGCCAGACTCTGTAGAGG	840
Qy	769	GTCGAAATTCGCCCCCTTCOG	GAAGATCCCGGTGCAACAGGAACCTCTGGCAATAGCC	828
Db	841	GTCGAAATTCGCCCCCTTCOG	GAAGATCCCGGTGCAACAGGAACCTCTGGCAATAGCC	900
Qy	829	AGGCTGCGGGTACTGTCCCA	GGGGTATGGCAGCTAGATGGCTTGTCTCTGCGCGGC	888
Db	901	AGGCTGCGGGTACTGTCCCA	GGGGTATGGCAGCTAGATGGCTTGTCTCTGCGCGGC	960
Qy	889	AAGGTAACACTGTCTGGCAGG	CAACAGACAGTCCCTGCCAGGCCACTTGTGCCACCA	948
Db	961	AAGGTAACACTGTCTGGCAGG	CAACAGTCCCTGCCAGGCCACTTGTGCCACCA	1020
Qy	949	GTGCCCCAGAAAGACGCCACT	GTGAATGAGCCACAAGATTTCCAGTTTGGTGGCAGGCCAC	1008
Db	1021	GTGCCCCAGAAAGACGCCACT	GTGAATGAGCCACAAGATTTCCAGTTTGGTGGCAGGCCAC	1080
Qy	1009	CCCAACCTCTGTCTCAGGTG	AGCACCTTGGGAGAGGTTCAGCTGCAAGCGTGTCTGTGG	1068
Db	1081	CCCAACCTCTGTCTCAGGTG	AGCACCTTGGGAGAGGTTCAGCTGCAAGCGTGTCTGTGG	1140
Qy	1069	GCTGACTCTTTGGGGCCCTT	CAAGCATGATATGCTGTAGTGAGATGAAAAACGGCGCTC	1128
Db	1141	GCTGACTCTTTGGGGCCCTT	CAAGCATGATATGCTGTAGTGAGATGAAAAACGGCGCTC	1200
Qy	1129	AACAACATCAGTCTGTGCTT	GGAAACCAAGTGGCTGTACACACTGCCCGCAAGATGGCC	1188
Db	1201	AACAACATCAGTCTGTGCTT	GGAAACCAAGTGGCTGTACACACTGCCCGCAAGATGGCC	1260
Qy	1189	TCCACGAGAGCTGTGCTCG	CTGGGAGAGGATTTGCTGCAAGACTTCCGATCACACCACTGT	1248
Db	1261	TCCACGAGAGCTGTGCTCG	CTGGGAGAGGATTTGCTGCAAGACTTCCGATCACACCACTGT	1320
Qy	1249	ATGCAGCTGTGGAACAGATG	ACAAATGGGATCGCTATGGGCTGCCCCCATGGAACAAGTAC	1308
Db	1321	ATGCAGCTGTGGAACAGATG	ACAAATGGGATCGCTATGGGCTGCCCCCATGGAACAAGTAC	1380
Qy	1309	ATCCACAGGGCGCTGGGTCT	TAGTATGGCTGTGCTGCCCTACTCTTTGGCTCGGGCGCTTTTC	1368
Db	1381	ATCCACAGGGCGCTGGGTCT	TAGTATGGCTGTGCTGCCCTACTCTTTGGCTCGGGCGCTTTTC	1440
Qy	1369	TTCTTCTCTCTTCTAAAAA	AGGACCGCAGGAAGCGGCGGTGCTCTCCGCACGGCCCTTG	1428
Db	1441	TTCTTCTCTCTTCTAAAAA	AGGACCGCAGGAAGCGGCGGTGCTCTCCGCACGGCCCTTG	1500
Qy	1429	CTCCTCCACTCCGCGGACG	AGCGGGCTACGAGAGCTGTGGTGGAGCACTGGGGCTCCGCG	1488
Db	1501	CTCCTCCACTCCGCGGACG	AGCGGGCTACGAGAGCTGTGGTGGAGCACTGGGGCTCCGCG	1560
Qy	1489	TTGAGCCAGATGCCACTCT	CGCGTGGCCGTGGACCTGTGTGAGCCCGCCGAGCTGAGCGC	1548

PRECIT.T 8

RESULTS 8
IIS-10-152-661-487

US-10-132-661-487
: Sequence 487. Application US/10152661

; sequence 487, Application 03/10
; Publication No. US20030022835A1: FUDICIALION NO: 0920
: GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

: APPLICANT: Onrust. Rene

APPLICANT: MURISON, JAMES G

APPLICANT: Kumble, Krishanand D

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 11000.1011C5

CURRENT APPLICATION NUMBER: US/10/152,661

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: 09/866,050

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 60/221,232

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: 60/206,650

; PRIOR FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: 09/3

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: PCT/NZ99/000511

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: 09/188,930

PRIOR FILING DATE: 1998-11-09

PRIOR APPLICATION NUMBER: 09/069,726

: PRIOR FILING DATE: 1998-04-29

; ERATOR FILING DATE: 1998-0
: NUMBER OF SEO ID NOS: 725; NUMBER OF SEQ ID NOS: 723
; SOFTWARE: FastSeq for Windows Version 4.0; SOF IAWAKE: FAS
; SEQ ID NO 487

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; SEQ ID NO 4
.   LENGTH: 2

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; LENGTH: 2.
. TYPE: DNA

TYPE: DNA
ORGANISM: Monera

; ORGANISM: MOU
IIS-10-152-661-487

	Query Match	95.6%;	Score 1933.6;	DB 6;	Length 2128;	
	Best Local Similarity	96.4%;	Pred. No. 0;			
	Matches 2018;	Conservative	0;	Mismatches	4;	Indels 72; Gaps 1;
QY	1	ATGCTGTGTCTTGTTCTGTCTGTCTTCTGGCAGCTCGGCCGGAACCCCTGTGGTGTGTCTCT	60			
DB	1	ATGCCTGTGTCTTGTTCTGTCTTCTGGCACATGGCCGGAACCCCTGTGGTGTGTCTCT	60			
QY	61	CTGGAGAGACTGATGAGCTCATGAGCACTGACGCTGTCTCTAAGGCTCTCTCTGCCAC	120			
DB	61	CTGGAGAGACTGATGAGCTCTAGGACACTGACGCTGTCTCTAAGGCTCTCTCTGCCAC	120			
QY	121	CTCTGGGATGGTAGCTGTCTGTCTGCTGGAGGCTCCAGTCTGCCCCAGGCCCTGTG	180			
DB	121	CTCTGGGATGGTAGCTGTCTGTCTGCTGGAGGCTTCAGTCTGCCCCAGGCCCTGTG	180			
QY	181	CTAGTGCCTACCSCCTGCAGACGAGACTGGTCTGAGGTGTCCAGAAGACAGATTGC	240			
DB	181	CTAGTGCCTACCSCCTGCAGACGAGACTGGTCTGAGGTGTCCAGAAGACAGATTGC	240			
QY	241	GCCCTCCGTGTCCGTGTGGTGGTCCACTTGGCCGTGATGGGCACATGGGCAGAGCCCTGAA	300			
DB	241	GCCCTCTGTGTCCGTGTGGTGGTCCACTTGGCCGTGATGGGCACATGGGCAGAGCCCTGAA	300			
QY	301	GAGCTGTGMAAGTCTGATTCAAGAACTCCAGAGTCTAGGAAACGCTCTCTCCAGGCCAG	360			
DB	301	GAGCTGTGMAAGTCTGATTCAAGAACTCCAGAGTCTAGGAAACGCTCTCTCCAGGCCAG	360			
QY	361	GTGGTGTCTCTTTCAGGCTTACCCATCCCGCTGTGCCCTGTGAGGCTCCAGGTG	420			
DB	361	GTGGTGTCTCTTTCAGGCTTACCCCATCCCGCTGTGCCCTGTGAGGCTCCAGGTG	420			
QY	421	CCCGCTGACCTGGTGAGGCTCTGGTCAAGTCCGTTGGGTCTGCGGTATTGTACTGTTTCGAG	480			
DB	421	CCCGCTGACCTGGTGAGGCTCTGGTCAAGTCCGTTGGGTCTGCGGTATTGTACTGTTTCGAG	480			
QY	481	GCTAGTCTTGGGCTCAGGTACAGATCTCTGCTTACAGAGCCGAGGTACCGAAGAG	540			
DB	481	GCTAGTCTTGGGCTCAGGTACAGATCTCTGCTTACAGAGCCGAGGTACCGAAGAG	540			
QY	541	CTCAACCTCACAGAGCTGCCT-----	564			
DB	541	CTCAACCTCACAGAGCTGCCTGACTCAGGGGTCTTGAAGTCCGGGACAGCATCCAG	600			
QY	565	-----GATGGTGAACAATGTCTCTCTGACA	588			
DB	601	AGCTGTGGGTCTTGCCCTCAATGTGTCTACAGATGTGTGACAAATGCTCTCTGACA	660			
QY	589	CTGGATGTCTCTGAGGACGAGCACTTTAGCTTTCTTA CTGTA CTTGGTCCAGTCCCGAT	648			
DB	661	CTGGATGTCTCTGAGGACGAGCACTTTAGCTTTCTTA CTGTA CTTGGTCCAGTCCCGAT	720			
QY	649	GCTCTCAAATCTTGTGGTACAAAACCTGCATGAGCTCAGAACCAATTAATTAAACCAAC	708			
DB	721	GCTCTCAAATCTTGTGGTACAAAACCTGCATGAGCTCAGAACCAATTAATTAAACCAAC	780			
QY	709	ACAGACCTTGTCTCCCTGCTCTGCAATTCAGGTGTGGTCTGAGCCAGACTCTGAGAGG	768			
DB	781	ACAGACCTTGTCTCCCTGCTCTGCAATTCAGGTGTGGTCTGAGCCAGACTCTGAGAGG	840			
QY	769	GTGCAATTCCTGCCCTTCGGGAGAGATCCCGGTGCACACAGGAACCTCTCGGCACATAGCC	828			
DB	841	GTGCAATTCCTGCCCTTCGGGAGAGATCCCGGTGCACACAGGAACCTCTCGGCACATAGCC	900			
QY	829	AGSCTCGGGTACTGTCTCCCAGGGGTATGGCAGCTAGATGGCTTGTCTGTCTGCCGGC	888			
DB	901	AGSCTCGGGTACTGTCTCCCAGGGGTATGGCAGCTAGATGGCTTGTCTGTCTGCCGGC	960			
QY	889	AAGGTAACACTGTGTGCGCAGCACCAGACACAGAGTCCCTGCGCAGCCAATTGTGCCACCA	948			
DB	961	AAGGTAACACTGTGTGCGCAGCACCAGACACAGAGTCCCTGCGCAGCCAATTGTGCCACCA	1020			

Qy	949	GTGCCCCAGAGAACGCCACTGTGGAATAGACCACAGAAATTTCAGTTTGGTGGCAGGACCTT	1080
Db	1021	GTGCCCCAGAGAACGCCACTGTGATATGATGACCAACAGATTTCAGTTTGGTGGCAGGCCAC	1080
Qy	1009	CCCAACCTCTGTGTCCAGGTGAGCACCTGGAGGAAGGTTTCAGCTGCAAGCGTGTCTCGTGG	1068
Db	1081	CCCAACCTCTGTGTCCAGGTGAGCACCTGGAGGAAGGTTTCAGCTGCAAGCGTGTCTCGTGG	1140
Qy	1069	GCTGACTCTTGGGGCCCTTCAAGATGATATGCTGTGTAGTGGAGATGAAAACGGGCTC	1128
Db	1141	GCTGACTCTTGGGGCCCTTCAAGATGATATGCTGTGTAGTGGAGATGAAAACGGGCTC	1200
Qy	1129	AACAAACATCAGTCTGTGCCCTTGGAAACCCAGTGGCTGTCACCACTGCCCAGCATGCC	1188
Db	1201	AACAAACATCAGTCTGTGCCCTTGGAAACCCAGTGGCTGTCACCACTGCCCAGCATGCC	1260
Qy	1189	TCCAGGAGCTGTCTGCTGTGGAGGAGGATTTGTCGAAGACTTCGATATCACCACTGTT	1248
Db	1261	TCCAGGAGCTGTCTGCTGTGGAGGAGGATTTGTCGAAGACTTCGATATCACCACTGTT	1320
Qy	1249	ATGCAGCTGTGAAACGATGACAACTGGATCGCTATGGCCCTGCCCATGACCAAGTAC	1308
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Qy	1309	ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTACTCTTGGCTGGGGCTTTTC	1368
Db	1381	ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTACTCTTGGCTGGGGCTTTTC	1440
Qy	1369	TTCTTCTCTTTTAAAAAGGACCCGAGAAAGCGCCCGTGGCTCCCGCACGGCCTTG	1428
Db	1441	TTCTTCTCTTTTAAAAAGGACCCGAGAAAGCGCCCGTGGCTCCCGCACGGCCTTG	1500
Qy	1429	CTCTCCACTCCGCGACGAGCGGGTACGAGCGTCTGTGGAGCACTGGCGTCCGCG	1488
Db	1501	CTCTCCACTCCGCGACGAGCGGGTACGAGCGTCTGTGGAGCACTGGCGTCCGCG	1560
Qy	1489	TTGAGCCAGATGCCACTTGCCTGGCCGTGACCTGTGGAGCGCCCGCGAGCTGAGCGCG	1548
Db	1561	TTGAGCCAGATGCCACTTGCCTGGCCGTGACCTGTGGAGCGCCCGCGAGCTGAGCGCG	1620
Qy	1549	CACGAGCCCTAGCCTGGTTCCACCAACAGCGACGCGGTATCTCTGACGAGGCTGGCGTG	1608
Db	1621	CACGAGCCCTAGCCTGGTTCCACCAACAGCGACGCGGTATCTCTGACGAGGCTGGCGTG	1680
Qy	1609	GTAATCTCTTCTTCTGCGCCCGCGCGCTGGCGAGTGTACGACAGTGGCTGCAGTCCAG	1668
Db	1681	GTAATCTCTTCTTCTGCGCCCGCGCGCTGGCGAGTGTACGACAGTGGCTGCAGTCCAG	1740
Qy	1669	ACAGTGGAGCCCGGGCCGATGACGCCCTCGCGCTGGCTCAGCTGGCTGTACCCGAT	1728
Db	1741	ACAGTGGAGCCCGGGCCGATGACGCCCTCGCGCTGGCTCAGCTGGCTGTACCCGAT	1800
Qy	1729	TTCTGTGAAGCCGGGGGACCCGGCCGCTACGTCGGGGTCTACTTCGAGGGGTGTGTGAC	1788
Db	1801	TTCTGTGAAGCCGGGGGACCCGGCCGCTACGTCGGGGTCTACTTCGAGGGGTGTGTGAC	1860
Qy	1789	CCAGACTCTGTGCGCTTCCCGGTTCCGCGTTCGCGCTCTTCTCTCTGCCCACGACGCTG	1848
Db	1861	CCAGACTCTGTGCGCTTCCCGGTTCCGCGTTCGCGCTCTTCTCTCTGCCCACGACGCTG	1920
Qy	1849	CCGGCTTTCTGTGATGACATGACAGGAGGCTGTCTCCACTTCGCGGGGACCCCGGAC	1908
Db	1921	CCGGCTTTCTGTGATGACATGACAGGAGGCTGTCTCCACTTCGCGGGGACCCCGGAC	1980
Qy	1909	CGGGTGAACGAGTGAACCAAGCGCTGCGGTCCGCTTGACAGCTGTACTTCTAGCTCG	1968
Db	1981	CGGGTGAACGAGTGAACCAAGCGCTGCGGTCCGCTTGACAGCTGTACTTCTAGCTCG	2040
Qy	1969	GAACCCCGGCTGCTGCGAGGAATGGACCTGGGACCTTGCACTACCTAGAA	2022
Db	2041	GAACCCCGGCTGCTGCGAGGAATGGACCTGGGACCTTGCACTACCTAGAA	2094

Db 1519 ATGCAGCTGTGAAACGATGACAAACATGGATCGCTATATGGGCTGCCCCATGAGCAAGTAC 1578
Qy 1309 ATCCACAGCGCTGGTCTCTAGTATGGCTGGCTCGCTACTCTTGGCTGCGCGCTTTTC 1368
Db 1579 ATCCACAGCGCTGGTCTCTAGTATGGCTGGCTCGCTACTCTTGGCTGCGCGCTTTTC 1638
Qy 1369 TTCTTCTCTCTTCTAAAGAACCGCAGGAAGCGGCCCGTGGCTTCCCGACGCGCTTG 1428
Db 1639 TTCTTCTCTCTTCTAAAGAACCGCAGGAAGCGGCCCGTGGCTTCCCGACGCGCTTG 1698
Qy 1429 CTCCTCCACTCCGCGACGAGCGGGCTACGAGCGTCTGGTGGGAGCACTGGCGTCCCG 1488
Db 1699 CTCCTCCACTCCGCGACGAGCGGGCTACGAGCGCTGGTGGGAGCACTGGCGTCCCG 1758
Qy 1489 TTGAGCCAGATCCCACTGCGCTGCGCGTGGACCTGTGGAGCGCGCGAGCTGAGCGCG 1548
Db 1759 TTGAGCCAGATCCCACTGCGCTGCGCGTGGACCTGTGGAGCGCGCGAGCTGAGCGCG 1818
Qy 1549 CAGGAGCCCTAGCTGGTTCACACCAAGCAGCGCGTATCTGCAGAGGGTGGCGTG 1608
Db 1819 CAGGAGCCCTAGCTGGTTCACACCAAGCAGCGCGTATCTGCAGAGGGTGGCGTG 1878
Qy 1609 GTAATCTCTCTCTCGCCCGCGCGCTGGCGCAGTGTACAGTGGCTGCAGCTCCAG 1668
Db 1879 GTAATCTCTCTCTCGCCCGCGCGCTGGCGCAGTGTACAGTGGCTGCAGCTCCAG 1938
Qy 1669 ACAGTGGAGCCCGGCGCGATGACGCCCTGCGCGCTGCTCAGCTGCTACCCGAT 1728
Db 1939 ACAGTGGAGCCCGGCGCGATGACGCCCTGCGCGCTGCTCAGCTGCTACCCGAT 1998
Qy 1729 TTCCTGCAAGCGCGGCGACCGCGCTACGTGCGGGTCTACTTCGAGGGGTGCTGCAC 1788
Db 1999 TTCCTGCAAGCGCGGCGACCGCGCTACGTGCGGGTCTACTTCGAGGGGTGCTGCAC 2058
Qy 1789 CCAGACTCTGTGCCCTCCCGCTTCGCGCTGCGCGCTCTCTCCCTGCGCGCAGCTG 1848
Db 2059 CCAGACTCTGTGCCCTCCCGCTTCGCGCTGCGCGCTCTCTCCCTGCGCGCAGCTG 2118
Qy 1849 CCGGCTTTCCTGGATGCACTGCAGGAGGCTGCTCCACTTCGCGGGGCGACCCCGGAC 1908
Db 2119 CCGGCTTTCCTGGATGCACTGCAGGAGGCTGCTCCACTTCGCGGGGCGACCCCGGAC 2178
Qy 1909 CGGGTGGAAAGTGAACCCAGCGCTGCGGTCCGCCCTTGAGCAGCTGTACTTCTAGCTCG 1968
Db 2179 CGGGTGGAAAGTGAACCCAGCGCTGCGGTCCGCCCTTGAGCAGCTGTACTTCTAGCTCG 2238
Qy 1969 GAAGCCCCCAGGCTGCTGCGAGGAATGGGACCTGGGACCCCTGCACACTAGAA 2022
Db 2239 GAAGCCCCCAGGCTGCTGCGAGGAATGGGACCTGGGACCCCTGCACACTAGAA 2292

RESULT 11
US-10-924-667-7
; Sequence 7, Application US/10924667
; Publication No. US2005009145A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/10/924,667
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/09/863,818
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (259)..()
; OTHER INFORMATION:
US-10-924-667-7

Query Match 95.6%; Score 1933.6; DB 9; Length 2314;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 2018; Conservative 0; Mismatches 4; Indels 72; Gaps 1;

Qy 1 ATGCTGTGTCTCTGGTTCCTGCTCTCTGTGGACATGCGCTGCGGCGGAAACCCCTGTGGTCTCTCT 60
Db 199 ATGCTGTGTCTCTGGTTCCTGCTCTCTGTGGACATGCGCTGCGGCGGAAACCCCTGTGGTCTCTCT 258

Qy 61 CTGGAGAGACTGATGGAGCCCTCAGACACATGCACGCTGCTCTCTAGGGCTCTCTCTGGCCAC 120
Db 259 CTGGAGAGACTGATGGAGCCCTCAGACACATGCACGCTGCTCTCTAGGGCTCTCTCTGGCCAC 318

Qy 121 CTCTGGGATGTGACGTGCTCTGCTGCTGGAAAGCCTCCAGTCTGCGCCAGGCGCTCTG 180
Db 319 CTCTGGGATGTGACGTGCTCTGCTGCTGGAAAGCCTCCAGTCTGCGCCAGGCGCTCTG 378

Qy 181 CTAGTGCTTACCCGCTGACAGCGGAGTGTGTCTGAGGTGTCCACAGAAACAGATTGC 240
Db 379 CTAGTGCTTACCCGCTGACAGCGGAGTGTGTCTGAGGTGTCCACAGAAACAGATTGC 438

Qy 241 GCCCTCCGTGTCCTGTGGTCCACTTGGCCGCTGCAATGGGCACTGGGCGAGGCTCGAA 300
Db 439 GCCCTCCGTGTCCTGTGGTCCACTTGGCCGCTGCAATGGGCACTGGGCGAGGCTCGAA 498

Qy 301 GAAGCTGGAAGTCTGATTCAAGAACTCCAGAGTCTAGGAAACGCTCTCTCCAGGCCCGAG 360
Db 499 GAAGCTGGAAGTCTGATTCAAGAACTCCAGAGTCTAGGAAACGCTCTCTCCAGGCCCGAG 558

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Thu Aug 17 14:34:40 2006

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; Sequence 74, Application US/10416442A
; Publication No. US20040171109A1
; GENERAL INFORMATION:
; APPLICANT: Haudenschield, Dominik
; APPLICANT: Roseley, Larry
; APPLICANT: Moseley, Timothy
; APPLICANT: Reddi, A. Hari
; TITLE OF INVENTION: IL-17 Receptor-Like Protein, Uses Thereof, and
; TITLE OF INVENTION: Modulation of Catabolic Activity of IL-17 Cytokines on
; TITLE OF INVENTION: Bone and Cartilage
; FILE REFERENCE: 023070-115511US
; CURRENT APPLICATION NUMBER: US/10/416,442A
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/247,134
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/271,197
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/328,904
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: WO PCT/US01/43855
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 74
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse IL-17RL cDNA with untranslated regions
US-10-416-442A-74
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Best Local Similarity 96.0%; Pred. No. 0;
Matches 2011; Conservative 6; Mismatches 5; Indels 72; Gaps 1;
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Db 2239 GAAGCCCCAGGCTGTGCGAGGAGTGGACCTGCGGAGCCCTGCGACCTGACACTAGAA 2292

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; Sequence 3, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc.feature
; LOCATION: (1)...(2022)
; OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 56.2%; Pred. No. 0;
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; Sequence 6, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
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; NAME/KEY: misc feature
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US-09-899-471-6

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GenCore version 5.1.9
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1113.4	55.1	2380	8	US-11-311-555-13 Sequence 13, Appl
3	1113.4	55.1	2380	8	US-11-311-561-13 Sequence 13, Appl
4	1113.4	55.1	2380	8	US-11-101-316-161 Sequence 161, App
5	1113.4	55.1	2380	8	US-11-311-554-13 Sequence 13, Appl
6	1113.4	55.1	2380	9	US-11-376-673-161 Sequence 161, App
7	610.2	30.2	2350	8	US-11-293-697-1517 Sequence 1517, Ap
8	552	27.3	1864	8	US-11-293-697-313 Sequence 313, App
9	467.2	23.1	1373	8	US-11-266-748A-15241 Sequence 15241, A
10	467.2	23.1	1373	8	US-11-266-748A-64946 Sequence 64946, A
11	467.2	23.1	1373	8	US-11-266-748A-67778 Sequence 67778, A
12	444.4	22.0	757	8	US-11-266-748A-218328 Sequence 218328, A
13	444.4	22.0	757	8	US-11-266-748A-239031 Sequence 239031, A
14	406	20.1	1000	8	US-11-266-748A-293048 Sequence 293048, A
15	406	20.1	1000	8	US-11-266-748A-344477 Sequence 344477, A
16	395.6	19.6	885	8	US-11-266-748A-361313 Sequence 361313, A
17	395.6	19.6	885	8	US-11-266-748A-387553 Sequence 387553, A
18	395.6	19.6	885	8	US-11-266-748A-444692 Sequence 444692, A
19	388.8	19.2	1061	8	US-11-266-748A-361314 Sequence 361314, A
20	388.8	19.2	1061	8	US-11-266-748A-387554 Sequence 387554, A
21	388.8	19.2	1061	8	US-11-266-748A-444693 Sequence 444693, A
22	376.2	18.6	923	8	US-11-266-748A-261876 Sequence 261876, A
23	376.2	18.6	923	8	US-11-266-748A-322393 Sequence 322393, A

ALIGNMENTS

RESULT 1

US-10-196-749-597
; Sequence 597, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 597
; LENGTH: 2380
; TYPE: DNA

Sequence 293049,
Sequence 344478,
Sequence 186516,
Sequence 361315,
Sequence 387555,
Sequence 444694,
Sequence 403105,
Sequence 474151,
Sequence 6434, Ap
Sequence 62257, A
Sequence 480243,
Sequence 364072,
Sequence 447451,
Sequence 177972,
Sequence 364146,
Sequence 388228,
Sequence 447525,
Sequence 42371, A
Sequence 364147,
Sequence 388229,
Sequence 447526,
Sequence 301303,

24 359 17.8 1000 8 US-11-266-748A-293049
c 25 359 17.8 1000 8 US-11-266-748A-344478
26 313 15.5 681 8 US-11-266-748A-186516
27 312.2 15.4 1144 8 US-11-266-748A-361315
28 312.2 15.4 1144 8 US-11-266-748A-387555
c 29 312.2 15.4 1144 8 US-11-266-748A-444694
30 304.6 15.1 1000 8 US-11-266-748A-403105
c 31 304.6 15.1 1000 8 US-11-266-748A-474151
32 297.4 14.7 571 8 US-11-266-748A-6434
c 33 288.4 14.3 494 8 US-11-266-748A-62257
c 34 275.2 13.6 1156 8 US-11-266-748A-480243
35 274.4 13.6 500 8 US-11-266-748A-364072
c 36 274.4 13.6 500 8 US-11-266-748A-447451
37 257 12.7 939 8 US-11-266-748A-177972
38 252.2 12.5 548 8 US-11-266-748A-364146
c 39 252.2 12.5 548 8 US-11-266-748A-388228
40 252.2 12.5 548 8 US-11-266-748A-447525
41 244.4 12.1 620 8 US-11-266-748A-42371
42 235.8 11.7 810 8 US-11-266-748A-364147
43 235.8 11.7 810 8 US-11-266-748A-388229
c 44 235.8 11.7 810 8 US-11-266-748A-447526
45 58.6 2.9 941 8 US-11-266-748A-301303

D	b	1493	CTACAAGACTGTCAGTCAAGCCAGTGCTGTGCAGCTATATGGACGATG---ACTTGGGAGCG	1549
Q	y	1282	CTATGGCCCTGCCCATGGAAGAATGATCCTCACAGGCGCTGGGTCTTAGTATGGCTGGCC	1341
D	b	1550	CTATGGCCCTGCCCATGGACAAATAATCCAAAGCGCTGGGCCCTCTGTGTGGCTGGCC	1609
Q	y	1342	TGCTACTCTTTGGTGGCGGCTTTTCTTCTTCTCTCTTCTAAAAGGACCGCAGGAAA	1401
D	b	1610	TGCCTACTCTTTGGCGTGGCGCTTTCCCTCATCTCTCTCTCAAAAAGGATCACGCGAAA	1669
Q	y	1402	-----GCGGCCGCTGGCTCCGCGACG	1422
D	b	1670	GGTGGCTGAGGCTTTGAACAACAGACGTCCTCGGGGGCGCGCCACAGGGCGCCGCG	1729
Q	y	1423	GCTTGTCTCTCACTCCGCGCAGGAGCGGGCTACGAGCGTCTGGTGGGAGCACTGGCG	1482
D	b	1730	GCTCTGCTCTCTTACTCAGCCGATGACTCGGGTTTCGAGGCGCTGGTGGCGGCCCTGGCG	1789
Q	y	1483	TCCGGCTTGAGCCAGATGCCACTGCGCGTGGCGGTGGAACCTGTGTGGAGCCGCGGAGCTG	1542
D	b	1790	TGGCCCTGTCCAGTCTGCGCTCGCGGTGGCGGTAGAACCTGTGTGGAGCCGTGTGTAACATG	1849
Q	y	1543	AGCGGCGACGAGCCCTAGCTGTGTCCACCACAGCGACCGCGTATCTCTGCAGGAGGGT	1602
D	b	1850	AGCGCGCAGGGGCGCGGTGGCTTTCACGCGCAGCGGGCGCCAGACCTCTGCAGGAGGGC	1909
Q	y	1603	GGCGTGTGAATCTTCTTCTTCGCGCGCGCGCTGTGCGCAGTGTACGAGTGGCTGCA-	1661
D	b	1910	GGCGTGTGGTCTTGCTTCTTCTCCCGGTGCGGTGCGGTGTGTGCAGCGAGTGGCTACAG	1969
Q	y	1662	-----GCTCCAAGACAGTGGAGCCGGGCGCATGACGCCCTCGCGGCTGGCTCAGC	1713
D	b	1970	GATGGGGTGTCCGGGCCCGGGCGCACGCGCCCGCACAGCGCTTTCGGGCTCGCTCAGC	2029
Q	y	1714	TGGGTGTACCCGATTCTCTGAAGCGCGGCGGACCGGCGCGCTACGTGGGGTCTACTTC	1773
D	b	2030	TGGGTGTCTCCCGAATTCTTTCAGGCGCGGGCGCCGCGCAGCTTCGGGCTCGCTCAGC	2089
Q	y	1774	GAGGGCTCTGCACCCAGACTCTGTGCCCTCCC CGTTCCGGTTCGGGTGCCCGCTCTTCTCC	1833
D	b	2090	GACAGGCTGCTCCACCCCGAGCCGCTACCGCGCTTTTCGACCGGTGCCGCTTTCACA	2149
Q	y	1834	CTGCCACCGAGCTGCGGCTTTCTCTGGATGCACTGCAGGAGGCGTGTCTCACTTCGCG	1893
D	b	2150	CTGCCCTCCCACTGCCAAGCTTCTTGGGGGCCCTGCAGAGCCTCGCGCCCGCGTTCC	2209
Q	y	1894	GGCGGACCCGCGGACCGGGTGGAAACGAGTGAACCAAGGCGCTCGGTTCGCGCTCGACAGC	1953
D	b	2210	GGCGGGCTCCAAAGAGAGCGGAGCAAGTGTCTCCGGGCGCTTTCAGCCAGCCCTGTGATAGC	2269
Q	y	1954	T-GTACTTCTAGCTCGGAGCCCGAGCTGTCTGCGAGGAATGGGACCTCTGGGAC	2005
D	b	2270	TACTTCATCCCCGGGGATCTCCCGCGCGGACGCGGGGTGGGACCGAGGCG	2322

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RESULT 3
US-11-311-561-13
; Sequence 13, Application US/11311561
; Publication No. US20060089917A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard

```

```

/ APPLICANT: Watanabe, Colin
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William
/ APPLICANT: Yansura, Daniel
/ TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
/ FILE REFERENCE: P1381R1C1P1(US)
/ CURRENT APPLICATION NUMBER: US/11/311,561
/ CURRENT FILING DATE: 2005-12-20
/ PRIOR APPLICATION NUMBER: US/09/747,259
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: US 09/311,832
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: US 60/172,096
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: PCT/US99/31274
/ PRIOR FILING DATE: 1999-12-30
/ PRIOR APPLICATION NUMBER: US 60/175,481
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: PCT/US00/04341
/ PRIOR FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: US 60/191,007
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: PCT/US00/07532
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: PCT/US00/15264
/ PRIOR FILING DATE: 2000-06-02
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 39
/ SEQ ID NO 13
/ LENGTH: 2380
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-11-311-561-13

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Query Match	55.1%;	Score 1113.4;	DB 8;	Length 2380;
Best Local Similarity	73.6%;	Pred. No. 3.2e-265;		
Matches 1541;	Conservative 0;	Mismatches 461;	Indels 91;	Gaps 6;

1	ATGCCTGTGTCCTGGTTCCTGCTGTCTTGGCACTGGGCGGAACCTGTGGTCTGCTCTCT	60
233	ATGCCTGTGCGCTGGTTCCTGCTGTCTTGGCACTGGGCGGAACCTGTGGTCTGCTCTCT	292
61	CTGGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGCTCTCTAGGCCCTCTCTGCGCAC	120
293	CTGGAGAGGCTTGTGGGGCCTCAGAGCGCTACCCACTGCTCTCGGGCCCTCTCTCGCCGC	352
121	CTCTGGGATGTGACGTGCTCTGCTGCTGGGAAGCCTCCAGTCTGCCCGCCAGGCCCTGTG	180
353	CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGTCTCGGGGCCCGCTG	412
181	CTAGTGCCTACCGGCTGCAGACGGAGCTGGTGTGAGGTGTCCACAGAAACAGAGATTGC	240
413	CTGGCGCCTACGCACTCTGCACACAGAGCTGGTGTGTGAGTGTCCAGAGGAGACCGACTGT	472
241	GCCTCTCCGTGTCCGTGTGGTGTGTCCACTTGGCCGTGTGCATGGGCATGTGGCGAGAGCTGAA	300
473	GACCTCTGTCTCGGTGTGGTGTCTCCACTTGGCCGTGTGCATGGGCATGTGGGAAGAGCTGAA	532
301	GAAGCTGGAAAGT-----CTGATTTCAGAACTCCAGGAGTCTAGGAACGCCCTCT	348
533	GATGAGGAAAAGTTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTTAGGATGCCCTCT	592
349	CTTCAGGCCACAGTGGTGTCTCTCTCCAGGCGCTACCCCATCGCCCGCTGTGCCCTGTG	408
593	CTTCAGGCCCAAGTGGTGTCTCTCTTCAGGCGCTACCCCTACTCTGCCCGCTGCGTCTGCTG	652
409	GAGGTCCAGTGTCCCGCTGACCTGGTGTGCAGCCTGTGTGTCGTTGGGTCTCGGCTATTT	468
653	GAGGTCCAGTGCCTGCTGCCCTTGTGTGAGTTTGGTTCAGTCTGTGGGCTCTCTGTGGTATAT	712
469	GACTGTTTCGAGGCTAGTCTTTGGGCTGAGGTACAGATCTGTGTCTCTACACGAAGCCCGAG	528

[illegible]

Db	1790	TCGGCCCTGTGCAGCTGCGCGTTCGCGGTGGCCGTTAGACCTGTGGAGCCGTCGTGAAC	1849
Qy	1543	AGCGCGCACGGAGCCCTAGCCTGTGTTCCACACACGACGACGCGTATCTCTGCAGGAGGGT	1602
Db	1850	AGCGCGCAGGGGCCGTGGCTTGCTTTACGCGCAGCGCGGCCAGACCCCTGACGAGGAGGC	1909
Qy	1603	GGCGTGGTAATCCTTCTCTCTCGCCGGCCGCTGGCGCAGTGT CAGCAGTGGCTGCA -	1661
Db	1910	GGCGTGGTGGTCTTGTCTTCTCTCCCGTGGCGGTGGCGCTGTGTCAGCGAGTGGCTACAG	1969
Qy	1662	-----GCTCCAGACAGTGGAGCCGGGCCCATGACGCCCTTCGCGCCTGGCTCAGC	1713
Db	1970	GATGGGCTGTCCGGCCCGGGCGCAGCGCCCGCACGACGCGCTTCGCGCTTCGCTCAGC	2029
Qy	1714	TGCGTGTCTACCAATTCGTGAAAGCGCGGGCGACCGGCGGCTACGTTCGGGGTCTACTTC	1773
Db	2030	TGCGTGTCTCCCACTTCTTTCAGGAGCGGGGCCCGCGAGCTACGTGGGGGGCTTCGCTTC	2089
Qy	1774	GAGGGGTGTGCACCCAGACTGTGTGCCCTCCCGCTTCGCGCTCGCGCCCGCTCTCTCC	1833
Db	2090	GACAGCTGTCTCACCGGAGCGCGTACCGGCCCTTTCCGCACCGTGC CGCTTCACAC	2149
Qy	1834	CTCGCCACGAGCTGCGGGCTTCTCTGATGCACTGCAGGGAGGCTGCTCCACTTCGGCG	1893
Db	2150	CTCGCCTCCCACTGCGAGACTTCTTGGGGGCCCTG CAGCAGCTTCGCGCCCGCGTTC	2209
Qy	1894	GGCGCACCCCGGACCGGGTGGAAACAGTGCACCGCGCTGCGGTTCGCGCTTCGGACAGC	1953
Db	2210	GGCGGGCTCCAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGC	2269
Qy	1954	T-GTACTTCTAGCTCGGAGCCCGACGGCTGCTCGAGGAAATGGAACTGGGAC	2005
Db	2270	TACTTTCATCCCGGGGACTCCCGCGCGCGGACGCGGGGTGGGACAGAGGGC	2322

RESULT 4

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US-11-101-316-161
; Sequence 161, Application US/11101316
; Publication No. US2006009657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 161
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-161

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Query Match 55.1%; Score 1113.4; DB 8; Length 2380;
Best Local Similarity 73.6%; Pred. No. 3.2e-265;
Matches 1541; Conservative 0; Mismatches 461; Indels 91; Gaps 6;


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; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/11/311,554
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 13
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-311-554-13

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Query Match	55.1%	Score 1113.4	DB 8	Length 2380
Best Local Similarity	73.6%	Pred. No. 3.2e-265		
Matches 1541	Conservative 0	Mismatches 461	Indels 91	Gaps 6
Qy	1	ATGCTGTGTCCTGGTTCCTGCTGCTGTGTCACATGGGCCGAAACCCGTGCGTCTCTCT	60	
Db	233	ATGCTGTGCGCCGTGTTCTTGTCTGTCTGTGGACATGGGCCGAAAGCCAGTGGTCTTCTTCT	292	
Qy	61	CTGGAGAGACTGATGGAGCCTCAGSACATGCACGCTCTCTCTAGGCCTCTCTCGCCAC	120	
Db	293	CTGGAGAGCCTGTGGGSCCTCAGACGCTACCCACTGCTCTCTCGGGCCTCTCTCTGCGC	352	
Qy	121	CTCTGGGATGTGACGTGCTCTGCTGCTGGAGACCTCCAGTCTGCCCCAGGCGCTGTG	180	
Db	353	CTCTGGGACATGTGACATCTCTGCTGCTCGGGACATCGTGTGCTCGGGGCCCCGTG	412	
Qy	181	CTAGTGCTTACCGCTGCAGACGGAGCTGTGTGAGGTGTCCACAGAACAGATTGC	240	
Db	413	CTGGCGCTACGCACCTGCAGACAGAGTGTGTCTGAGTGTCCAGAGGAGACCGACTGT	472	
Qy	241	GCCCTTCGTGTCGTGTGGTGGTCCACTTGGCCCGTGCATNTGGGCATCTGGGCAGAGCCTGAA	300	
Db	473	GACCTCTGTCTGCGTGTGGTGTCCACTTGGCCCGTGCATNTGGGCATCTGGGAAGAGCCTGAA	532	

Db	1610	 TGCTACTTTTGGCGTGGCTTTCCTCATCTCTCTCAAAAAGGATCACGCGAAA	1669
Qy	1402	-----GCGGGCCGTGGCTCCCGCAGC	1422
Db	1670	GGGTGGCTGAGGCTCTTGAAAACAGGACGTCCGTCGGGGCGCGCCGCMGGGGCCGCGG	1729
Qy	1423	GCCTTCCTCTCACATCCGCGACGAGGAGCGGGTACGAGCGTCTGTGGAGACATGCGG	1482
Db	1730	GCTCTGCTCTCTACTACGCGGATGACTCGGGTTTCGAGCGCTGTGGGCGCCCTTGCG	1789
Qy	1483	TCGCGCTTGAGCCAGATGCCATGCGCGTGGCGGTGGACCTGTGAGCCGCGCGAGCTG	1542
Db	1790	TCGGCCCTGTGCGAGCTGCCGTGCGCGTGGCGGTAGACCTGTGGAGCCGTGTAACCTG	1849
Qy	1543	AGCGCGCACGGAGCCCTAGCTGGTTCCACACGAGGACGCGCTATCTCTGCAGGAGGT	1602
Db	1850	AGCGCGAGGGGCGCGTGGCTTGTTGTTTTCACGCCAGCGGGCCAGACCTTCGACGAGGCG	1909
Qy	1603	GGCGTGGAATCCTTCTCTTCGCCCGCGCGTGGCGAGTGTGAGCAGTGGCTGCA-	1661
Db	1910	GCGTGTGTGCTTGTCTTCTCTCCGCGTGGCGTGTGCGAGCAGTGGCTACAG	1969
Qy	1662	-----GCTCCAGACAGTGGAGCCCGGCGCGCATGACGCCCTCGCGCGCTGGCTCAGC	1713
Db	1970	GATGGGGTGTCCGGGCGCGGGCGCACGGGCCCGACGCGCTTCGCGGCTCGCTCAGC	2029
Qy	1714	TGGTGCTTACCCGATTTCTTGCAAGGCGGGCGACCGGCGCTACGTCGGGGTCTACTTC	1773
Db	2030	TGCGTGTCTCCGACTTCTTGCAAGGCGGGCGCGCGCGGCGAGCTACGTGGGGGCTGCTTC	2089
Qy	1774	GACGGGCTGTGCAACCCAGACTCTGTGCGCTCTCCCGTTCGCGTGGCGCCCGCTCTCTCC	1833
Db	2090	GACAGGCTGTCTCCACCCCGGACGCGGTACCGCGCCCTTTTCGCGCACCGTGCCGCTTTCACA	2149
Qy	1834	CTGGCCACGCGAGTCGCGGCTTTTCTCGATGCACTGACGAGGAGCTGCTCCACTCCGCG	1893
Db	2150	CTGGCTCTCCAATCTGCCAGACTTCTTGGGGGCGCTTCGACAGCGCTCGCGCCCGCGTTC	2209
Qy	1894	GGGCGACCCGCGGACCGGGTGGAAAGAGTGAACCCAGCGCTGCGGTCGCGCTTGAGCAGC	1953
Db	2210	GGGCGGCTCAAGAGAGAGCGAGGAGTGTCCCGGCGCTTCAGCCAGCGCTTGATAGC	2269
Qy	1954	T-GTACTTCTAGCTCGGAAGCCCCAGGCTGTGCGAGGAATGGACCTGGGAC	2005
Db	2270	TACTTCAATCCCGCGGAGCTCCGCGCGGGAACGCGGGGTGGGACAGAGGCG	2322

RESULT 6
US-11-376-673-161
; Sequence 161, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; FILE REFERENCE: P3230R1C185C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 161

	Query Match	55.1%	Score 1113.4	DB 9	Length 2380
	Best Local Similarity	73.6%	Pred. No. 3.2e-265		
	Mismatches	0	Mismatches 461	Indels 91	Gaps 6
	Mismatches 1541	Conservative			
QY	1	ATGCTGTGTCCTGGTTCCTGCTCTGTCACCTGGCCGGAACCCCTGTGGTCTGCTCT	60		
DB	233	ATGCTGTGTCCTGGTTCCTGCTCTGTCACCTGGCCGGAACCCCTGTGGTCTGCTCT	292		
QY	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGCAACGCTGCTCTTAGGCTCTCTCTGGCAC	120		
DB	293	CTGGAGAGCCTGTGGGSCCTCAGGACGCTACCCACTGCTCTCCGGGCTCTCTCTGGCGC	352		
QY	121	CTCTGGATGTGACGTGCTCTGCTGCTCGGAGCCTCCAGTCTGCCCCAGGCGCTGTG	180		
DB	353	CTCTGGGACAGTGACATACCTCTGCTGCTGGGACATCTGTCCTCTGCTCCGGGCCCGTG	412		
QY	181	CTAGTGCCTTACCCGCTCTCAGACGGAGCTGGTGTGAGGTTCCACAGAACACAGATTGC	240		
DB	413	CTGGCGCCTACGCACCTCCAGACAGAGCTGGTGTCTAGGTGCCAGAGAGACCGACTGT	472		
QY	241	GCCTCCGHTCCGTGGTGGTTCACCTGGCCGTCATGGGCATCTGGGCAGAGCCTCAA	300		
DB	473	GACCTCTGTCTGCTGTGGCTGCACCTGGCCGTCATGGGCATCTGGGACCTGGAGAGCCTGAA	532		
QY	301	GAAGCTGGAAAGT-----CTGATTCAGAACTCCAGGAGCTTAGGAAACGCTCT	348		
DB	533	GATGAGGAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGAGCCTTAGGAAATGCCTCT	592		
QY	349	CTCCAGGCCAGGTGGTGTCTCTTCCAGGCTACCCATCGCCGCTGTGCCCCCTGCTG	408		
DB	593	CTCCAGGCCAAAGTCGTGTCTCTTCCAGGCTACCCCTACTGCCCCGCTCGCTCTGCTG	652		
QY	409	GAGTCCAGGTGCCGCTGCACCTGGTGCAGCTGGTTCAGTCCGTGGGTTCTGCGGTATTT	468		
DB	653	GAGTCCAGGTGCCGCTGCCCTTGTGCAGTTTGGTCACTCTGGGCTCTGTGGTATAT	712		
QY	469	GACTGTTCCAGGCTAGTCTTGGGGCTGAGGTACAGATCTGCTCTCTACAGAACGCCAGG	528		
DB	713	GACTGTTCCAGGCTGCCCTTAGGGAGTGAAGTACGAACTGTGCTCTATCTCAGCCAGG	772		
QY	529	TACCAGAAAGCTCAACCTCACACAGCAGCTGCCT-----	564		
DB	773	TACGAGAGGACTCAACACACACAGCAGCTGCCTGCCCTGCGCTCAACGCTGTCA	832		
QY	565	---GATGGTGACAATGTCCCTTTGACACTGGATGTCTCTGAGGAGCAGACCTTTAGCTTC	621		
DB	833	GCAGATGTTGACAAAGTGCATCTGGTCTTGAATGTCTCTGAGGAGCAGCACTTCGGCCTC	892		
QY	622	TTACTGTACTGCGTCCAGTCCCGGATGCTCTCAAATCCTTGTGTGTACAAAACTTGACT	681		
DB	893	TCCTGTGTACCTGGAACTCAGGTTCAGGGCCCCCAAAACCCCGGTGGCACAAAACCTGACT	952		
QY	682	GGACCTCAGAACATTAATTTAAACCAACAGACCTGGTTCCTGCTCTGCTCATTCAGGTG	741		
DB	953	GGACCGCAGATCATTAATTTGAAACCAACAGACCTGGTTCCTGCTGTGTATTCAGGTG	1012		
QY	742	TGGTTCGTAGACCAAGACTCTGAGAGGTCGAAATCTGCCCCCTTCCGGGGAAGATCCCGGT	801		
DB	1013	TGGGCTCTGGAACCTGTACTCCGTTAGGACGAAATCTGCCCTTTCAGGGAGGACCCCGC	1072		
QY	802	GCACACAGAACCTCTGGCACATAGCCAGGCTGCGGGTATCTGTCCCAGGGGTATGGCAG	861		
DB	1073	GCAACACAGAACCTCTGGCAAGCCGCCAGCTGCGACTGTCTGACTGACCTCTGCAGAGCTGGCTG	1132		
QY	862	CTAGATGGCCCTGCTGTCTGCCGGCAGAGTAACTGTCTGTGGCAGGACACAGAACAG	921		
DB	1133	CTGACGACACGCTGCTGCTGCCCGCAGAGCGGCATCTGTGCTGCGGGCTCCGGGTGGG	1192		

Db 869 CAGATGTCAGAACGTCATCTGTTCTGAATGTCTCTGAGGACGACATCTCGGCGCTCT 928
 QY 623 TACTGTACCTGCGTCAGTCCGAGTCTCTCAATCTTGTGTGTCACAAAACCTGACTG 682
 Db 929 CCCTGTACTGGAATCAGGTTCAGGGCCCCCMAAACCCCGGTGGCACAANAACCTGTGTA 988
 QY 683 GACCTCAGAAACATTTACTTTAAACACACAGACTGTGTTCCCTCTGCAATTCAGGTGT 742
 Db 989 GGCCTC---CCCTTCCCAAGTCATCTCCACTGTAGGCCGATGCTGTGCAAAAGACGC 1045
 QY 743 GGTGCTAGAGCCAGACTCTGAGAGGTGCAATTTCTGCCCCCTTCGGGAGAGATCCCGGTG 802
 Db 1046 AGTGCCATATCAGAGAGGATCTTTGAAGAGGACTCACCCCAAGCAAGGGAAAATTTGACTG 1105
 QY 803 CACACAGGAACTCTGGCACATAGCCAGGCTGCGGGTACTGTCTCCCAAGGGGTATGGCAGC 862
 Db 1106 GACCGCAGATCATTTACCTTGAACACACAGACCTGGTTCCCTGCTCTGTATTCAGGTG- 1164
 QY 863 TAGATGCGCTTGTCTGTCTGCGGGCAAGTAAACACTGTGTGTCGACGACGACACAGACAGA 922
 Db 1165 TGGCTCTGGAACTGACTCTCGTTAGGACGAACATCTGCCCTTTACGGGAGGACCCCGC 1224
 QY 923 GTCCCTGCACGCACTTGTGCCACAGTGCCCGAGAGAAACGCGCACTGTGATGAGCCAC 982
 Db 1225 GCACACAGAACTCTTGCAAGCGCGGACTGCGGACTGTGACCCCTGACAGCTGGCTG 1284
 QY 983 AAGATTTCCAGTTGGTGGCAGGCGCACCCCAACCTCTGTGTCCAGGTGAGCACTGGGAGA 1042
 Db 1285 CTGAGCGCACGTCCTGCTGCCCGCAGAGGCGCACTGTCTGGCGGCTCCGGGTGGG 1344
 QY 1043 AGGTTACGTCGAACGCTGCTGTGGGTGACTCTCTTGGGGCCCTTCAAGATGATATGC 1102
 Db 1345 GACCCCTGCCAGCACTGTCTCCACCGCT--TTCTGGGAGAACGTCACTGTGACAAAGG 1402
 QY 1103 TGTAGTGAGATGAACACCGGCTCAACACACATCAGTCTGTGCCCTTGGAAACCCAGTG 1162
 Db 1403 TTCTCG-----AGTTCCCATTTGCTGAAAGGCCACCTTAACCTCTGTGTTACGA 1451
 QY 1163 GGTGTACACCACTGCCAGCATGGCTCCACAGAGCTGTCTGCGCTGGGAGAGAGTTGC 1222
 Db 1452 GGTGAACAGCTCGGAGAGCTGCAGCTGCAGAGTGTCTTGTGGGTGTATGG----- 1504
 QY 1223 TGCAAGACTTCGGATCACACAGTGTATGCAGCTGTGGAAACGATGACAAACATGGGATCGC 1282
 Db 1505 -----GACGATCACTTGGAGGCG 1523
 QY 1283 TATGGCCTGCCCCATGACAAAGTATACATCCAGGCGCTGGGTCTCTAGTATGGCTGGCT 1342
 Db 1524 TATGGCCTGCCCCATGACAAATATACATCCAAAGCGCTGGGCCCTCTGTTGGCTGGCT 1583
 QY 1343 GCCTACTCTGGCTGGGCGCTTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1401
 Db 1584 GCCTACTCTTCTGGCTGGGCTTTCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1643
 QY 1402 -----GCGGCCCTGGCTCTCCCGCAGG 1423
 Db 1644 GGTGGCTGAGGCTCTTGAACAGAGAGTCCGCTCGGGGGCGGCGCCAGGGGCGCGCGG 1703
 QY 1424 CTTTGTCTCTCACTCCGCGCAGAGCGGGCTTACAGCGCTTGTGTGGAGCACTTGGGCT 1483
 Db 1704 CTCCTGCTCTTACTCAGCCGATGACTCGGGTTTCGAGCGCTTGTGTGGGCGCTCTGGCT 1763
 QY 1484 CCGGTTGAGCAGATGCCACTGCGGCTGGCGGTGAGACCTGTGGAGCGCGCCGAGCTGA 1543
 Db 1764 CGGCCCCGTGTCAGCTGCGGCTGCGGCTGGCGGTGAGACCTGTGGAGCCCTCTGTAATGA 1823
 QY 1544 GCGCGCAGGAGCCCTAGCTGTGTTCCACACACAGCGACCGGATATCTCTGACGAGGGGTG 1603
 Db 1824 GCGCGCAGGGGCGGCTGGCTTGGTTTTCACGCGCAGCGCGCCAGACCTCTGACGAGGGG 1883
 QY 1604 GGTGTGAATCTCTTCT 1661

Db 1884 GCGTGTGTGTCTGTCTCTTCTCTCCCGGTGCGGTGCGGTGCGAGGAGTGCTACAGG 1943
 QY 1662 -----GCTCCAGACAGTGGAGCCCCGGGCGGATGACGCCCCCTCGCGGCTGCTCAGCT 1714
 Db 1944 ATGGGTGTGTCGGGCGCGGGCGGACGCGCCGACACGCTTCCGCGGCTCTGCTCAGCT 2003
 QY 1715 GCGTGTCTACCCGATTTCTTGCAGAGCGCGGCGGACCGGCGCTACGTCGGGGTCTACTTCG 1774
 Db 2004 GCGTGTCTGCCCCGACTTCTTGCAGGGCGCGGGCGCCGCGAGCTACGTCGGGGCTGCTTCG 2063
 QY 1775 ACGGGCTGTGCAACCCAGACTCTGTGCCCCCTCCCGTTTCGCGTTCGCGCCCTCTTCTCCC 1834
 Db 2064 ACAGGCTGTCTCCACCCGACGCGGTACCCGCCCCCTTTTCCGACACCGTCCGCTCTTCACAC 2123
 QY 1835 TGCCCAAGCAGCTGCGGGCTTCTCTGATGACACTGCAGGGAGGCTGTCTCCACTTCCGCGG 1894
 Db 2124 TGGCCTTCCCAACTGCGAGACTTCTTGGGGGCTCTGCAGAGCCTTGGCGCCCCCGGTTCCG 2183
 QY 1895 GCGGACCCGCGGACCGGGTGGAAACGAGTGAACCCAGGCGTTCGCGTCCGCTTGACAGCT 1954
 Db 2184 GCGGCTTCCAGAGAGAGCGGAGCAAGTGTCCCGGCCCCCTTCAGCCAGCCTCGATAGCT 2243
 QY 1955 -GTACTTCTAGCTCGGAAGCCCCCAGGCTGTCTGCGAGGAATGGGACCTGG 2002
 Db 2244 ACTTCCATCCCGGGGACTTCCCGCGCCGGGACGCGGGGTGGGACCAAG 2292

RESULT 8

US-11-293-697-313
 ; Sequence 313, Application US/11293697
 ; Publication No. US20060105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293,697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIOR APPLICATION NUMBER: US/10/108,260
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 313
 ; LENGTH: 1864
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-293-697-313

Query Match 27.3%; Score 552; DB 8; Length 1864;
 Best Local Similarity 74.5%; Pred. No. 1.8e-126;
 Matches 739; Conservative 0; Mismatches 240; Indels 13; Gaps 3;

QY 1024 CAGGTGAGCAGCTGGGAGAGGTTTTCAGCTGCAAGCGTCTCTGTTGGGTGACTCTCTTGGGG 1083
 Db 821 CAGGTGAGCAGCTGGGAGAGCTGCAGCTGCAGGAGTCTTGTGGGTGACTCTCTTGGGG 880
 QY 1084 CCCTTCAAGAGATATATGCTTTAGTGGAGATGAACCGGCTTCAACAAACATCATCTC 1143
 Db 881 CCTCTCAAGAGATATGCTTACTTGTGGAGACAGAGGCCCCCAGGCAACAGATCCCTC 940
 QY 1144 TGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCCCAGCATGGCTCCACGAGAGCTGCT 1203
 Db 941 TGTGCTTGGAAACCCAGTGGCTGTACTTCACTACCCAGAAAGCCTCCACGAGGCGAGCT 1000
 QY 1204 GCGCTGGAGAGGAGTTTCTGCAAGACTTCCGATCACACGATGTATGATGAGTGGAC 1263
 Db 1001 GCGCTTGGAGAGTACTTACTACAGACCTGAGTCCAGGCGAGTGTCTGAGCTATGGGAC 1060
 QY 1264 GATGACACATGGGATCCGCTATGGCTGCCCCATGGGACAAATACATCCACAGGCGCTG 1323
 Db 1061 GATG---ACTTGGAGGCGCTATGGGCTTGGCCCATGGACAAATACATCCACAGGCGCTG 1117
 QY 1324 GTCCTAGTATGCTGCGCTGCTACTCTTGGCTGCGGCGCTTTTCTTCTCTCTCTTA 1383

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Db 1118 GCCCTGCTGGCTGGCTGCTACTCTTTGGCCGCTGGCTTTCCTCATCTCTTCTC 1177
Qy 1384 AAAAAGACCCAGAGAAAGCGCCGCTGCTCCCGACGCGCTTCTCTCCACTCCGCC 1443
Db 1178 AAAAAGATCACCGAAAGCGCCGACAGGGCGCGGCTCTCTCTACTACGCC 1237
Qy 1444 GACGAGCGGGCTACGAGGCTTGTGTGGAGCACTGGGCTCGGCTTGGAGCAGATGCCA 1503
Db 1238 GATGACTCGGCTTTCGAGCGCTGTGTGGCGCCCTGGCCCTGTGCCAGCTGCCG 1297
Qy 1504 CTGGCGTGGCGCTGGACCTGTGGAGCGCGCGAGCTGAGCGCGACCGAGCCCTAGCC 1563
Db 1298 CTGGCGTGGCGTAGACTGTGGAGCGCTGTGAACTGAGCGCGAGCGCGCGTGGCT 1357
Qy 1564 TGGTTCCACACCGACGCGCTATCTGACGAGGGTGGCTGTAATCTTCTCTTC 1623
Db 1358 TGGTTTACGCGCGAGCGCGCGCAGACCTTCGAGGAGGCGCGGTGTGCTCTTCTTC 1417
Qy 1624 TGGCGCGCGCGTGGCGAGTGTGACGAGTGGCTGCA-----GCTCCAGACAGTG 1674
Db 1418 TCTCCCGGTGGGTGGCGCTGTGACAGAGTGGCTTACAGGATGGGTGTCCGGGCGCGG 1477
Qy 1675 GAGCCCGCGCGCATGACGCCCTCGCCGCTGGCTGAGCTGCTGCTACCGGATTTCTG 1734
Db 1478 GCGCAGCGCGCGACGAGCTTCCGCGCTGCTGCTGAGTGGTGTGCTCCGACTTCTTG 1537
Qy 1735 CAAGCGCGCGCGACCGCGCTAGCTCGGGGTCTACTTCGACGGGCTGCTGACCCAGAC 1794
Db 1538 CAGGCGCGCGCGCGCGAGCTAGCTGGGGGCTGCTTCGACAGGCTGCTCCACCGGAC 1597
Qy 1795 TCTGTGCTCCGCTTCCGCTGCGGCTGCGCGCTTCTCTCCCTGCGCAGCAGCTGCGGCT 1854
Db 1598 GCCGTACCCGCGCTTTTCCGACCGTGCCTCTTTCACACTGCCCTCCAACTGCCAGAC 1657
Qy 1855 TTCCTGATGACATGACGAGGCTGCTCCACTTCCGCGGCGCGACCGCGCGCGGTG 1914
Db 1658 TTCCTGGGGCCCTGACAGACCTCGCGCCCGGCTTCGCGCGGCTCAAGAGAGAGCG 1717
Qy 1915 GAACGAGTACCCAGGCGCTCGGCTCGCCCTCGGACAGCT-GTACTTCTAGCTCGGAAGC 1973
Db 1718 GAGCAAGTGTCCCGGCGCTTCAGCAGCCCTTCAGCAGCCCTGGATAGCTACTTCCATCC 1777
Qy 1974 CCCAGGCTGCTGCGAGGATGGGACCTGGGAC 2005
Db 1778 CCCGCGCGGACGCGGGGTGGGACGAGGCG 1809
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RESULT 9

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US-11-266-748A-15241/c
; Sequence 15241, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15241
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc feature
; LOCATION: (1237)..(1245)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-15241

Query Match      23.1%; Score 467.2; DB 8; Length 1373;
Best Local Similarity 65.2%; Pred. No. 1.5e-105;
Matches 903; Conservative 0; Mismatches 288; Indels 193; Gaps 7;

Qy 1 ATGCTGTGTCTGTTTCTGCTGCTTGTGGCACTGGGCGGAAACCTGTGTGTCTCT 60
Db 1193 ATGCTGTGCGCTGGTTCTTGTGTCTTGTGGCACTGGGCGGAAAGCCAGTGTCT 1134
Qy 61 CTGGAGAGACTGATGGAGCCTCAGACACTGCACTGCTCTCTAGGCTCTCTCTGCCAC 120
Db 1133 CTGGAGAGGCTTGTGGGCGCTCAGAGCGCTACCCACTGCTCTCCGGGCTCTCTCTGCCGC 1074
Qy 121 CTCTGGGATGTGTGAGCTGCTCTGCTGCTGCTGGAAGCCTCCAGTCTGCCCCAGGCCCTGTG 180
Db 1073 CTCTGGGACAGTGTACATACTCTGCTGCTGCTGGGACATGCTGCTCTCGGGCCCCGTG 1014
Qy 181 CTAGTGTCTACCCGCTGACAGACGAGCTGTGTGTGAGGTGTCCACAGAGACAGATTGC 240
Db 1013 CTGGCGCTACGCACTTGACAGAGAGCTGTGTGTGTGAGGTGTCCAGAGAGAGACCGACTGT 954
Qy 241 GCCCTCCGTGTCCGTGTGGTGTGCTTCCACTTGGCGGTGATGGGCACTGGGCGAGGCTGAA 300
Db 953 GACCTGTGTGTGCGGTGGCTGTCCACTTGGCCGTGCAT----- 915
Qy 301 GAAGCTGGAAGTCTGATTAGAACTCCAGGAGTCTAGGAAGCGCTCTCTCCAGAGCCCCAG 360
Db 914 -----GCCCTCTCCAGGCGGCA 897
Qy 361 GTGTGTCTCTCTTCCAGGCTTACCCCATCCCGCTGTGCTGCTGCTGAGAGTCCAGGTG 420
Db 896 GTGTGTCTCTCTTCCAGGCTTACCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
Qy 421 CCCGTGACCTGTGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 836 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Qy 481 GCTAGTCTTGGGCTGTAGGTACAGATCTGTGCTTACAGAAAGCCAGGTACCCAGAAAGAG 540
Db 776 GCTGCTCTAGGAGTGTAGGTAGGATCTGTGCTTATATATATATATATATATATATATATAT 717
Qy 541 CTCACCTCTACACAGAGCTGCTGAGTGTGCAATGTCTTGTGACACTGATGTCTCT 600
Db 716 CTCACGACACACAGAGCTGCTG-----CCCTGCTGCTGCTCAACGTGCA 670
Qy 601 GAGGACGAGGACTTTAGCTTCTTACTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 669 GCAGATGGTGAACAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Qy 661 TTGTGTGTACAAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 609 TCCCTGTACTGGAATCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Qy 721 -CCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
Db 549 CCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
Qy 780 CCCCTTCCGGGAAGATCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
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/	PRIOR APPLICATION NUMBER:	EP 04105483.4
/	PRIOR FILING DATE:	2004-11-03
/	PRIOR APPLICATION NUMBER:	EP 04105507.0
/	PRIOR FILING DATE:	2004-11-03
/	PRIOR APPLICATION NUMBER:	EP 04105485.9
/	PRIOR FILING DATE:	2004-11-03
/	PRIOR APPLICATION NUMBER:	EP 04105484.2
/	PRIOR FILING DATE:	2004-11-03
/	PRIOR APPLICATION NUMBER:	US 60/662,276
/	PRIOR FILING DATE:	2005-03-14
/	PRIOR APPLICATION NUMBER:	US 60/700,293
/	PRIOR FILING DATE:	2005-07-18
/	NUMBER OF SEQ ID NOS:	483996
/	SOFTWARE:	PatentIn version 3.3
/	SEQ ID NO	239031
/	LENGTH:	757
/	TYPE:	DNA
/	ORGANISM:	Homo Sapiens
/	US-11-266-748A-239031	

Query Match		22.0%; Score 444.4; DB 8; Length 757;
Best Local Similarity		76.7%; Pred. No. 5e-100;
Matches 557; Conservative		0; Mismatches 166; Indels 3; Gaps 1

QY	679	ACTGGACCTCAGAACATTA	CTTTAAACCACACAGACCTG	TTCCTTCCCTCGCATTCAG	738
Db	1	ACTGGACCGCAGATCA	TACTTGAAACCACACAGACCTG	TTCCTTCCCTCGCATTCAG	60
QY	739	GTCGTGTCGTAGAGCCAG	CACACTCTGAGAGGTCGAATT	TCTGCCCTTCCGGGAAGATCCC	798
Db	61	GTCGTGCCTCTGGAACT	CTGACTCGGTAGSACGAACA	TCTGCCCTTCCGGGAGACCCC	120
QY	799	GGTGCA CACAGAACTCT	GGCACATAGCCAGGCTGGG	GTACTGTCCCCAGGGGTATGG	858
Db	121	CGGCGACACCAAGAACT	CTGGCAAGCGCCGACTGCG	CACTGTGACCTTCAGAGCTGG	180
QY	859	CAGCTAGATGCGCCTTG	CTGTCTGCGCGGCAAGGTAA	CACATGCTGTGCGAGGACCA	918
Db	181	CTGCTGGAGCGCACCGT	GTCTGCTGCGCCGCGAAGCG	GCGCACTGTCTGCGGGCTCCG	240
QY	919	CAGAGTCCCTGCGACCCA	CTTTGTGCACTTGTGCACTCT	GTGTCCAGGTGAGCACCTGG	1038
Db	241	GGGGACCCCTGCGACCCA	CTGTCCTCCACCGCTTCTCT	GGGAGAAGCTCACTGTGGACA	300
QY	979	CCACAAGATTTCCAGTT	GGTGCGCAGGCCACCCCAAC	CTCTGTGTCCAGGTGAGCACCT	360
Db	301	GTTCTCGAGTTTCCCA	TTGCTCAAAGGGCCACCCTAA	CCCTCTGTGTCTCCTCAAGAC	420
QY	1039	GAGAAGGTTTCAGCTG	CAAGCGTGCTCTGTGGGTG	CACTCTTGGGGCCCTTCAAG	1098
Db	361	GAGAAGCTGCAAGCTG	CAAGGAGTGCTGTGGGGTGA	CTCCCTGCGGGCTCTCCTCA	480
QY	1099	ATGCTGTTAGTGAGATA	AGAAAACCGGCTCAACAACA	TCATCACTGTGCTTGGAA	1158
Db	421	GTGCTACTGTTGGAGAC	AAGGGCCCAAGAACAGAGAT	TCCTCTGTGCTTGGAA	480
QY	1159	AGTGGCTGTACACCACT	GCCAGCATGGCCCTCCACG	AGAGTCTGCTGCGGAGGAG	1218
Db	481	AGTGGCTGTACTTCACT	TACCACCAAGGCTCCACG	AGGCACTGCGCTTGGAGTAG	540
QY	1219	TTGCTGCAAGACTTCG	ATCACCAAGTGTATGCACT	GTGTGAAACGATGCAAC	1278
Db	541	TTACTACAAGACCTG	CAGTCAGGCCAGTGTCTG	CAGCTATGGAGCAATGG	597
QY	1279	TGCGTATGGCCCTG	CCCCATGGCAAGTACATCC	ACAGCGCTGGGTCTTAGT	1338
Db	598	GCCTATGGGCCCTG	CCCCATGGCAAAATACAT	CCACAGCGCTGGGCCCTG	657
QY	1339	GCCTGCTACTCTTTG	CTCGGGCTTTTTCTTCTTC	CTCTTCTAAAAAGGACCG	1398
Db	658	GCCTGCTACTCTTTG	COGCTCGGCTTTTCCCT	CTCATCTCTCTCAAAAAG	717
QY	1399	AAAGCG	1404		

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Db          ||||| 718 AAAGG 723

RESULT 14
US-11-266-748A-293048
; Sequence 293048, Application US/11266748A
; Publication NO. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/562,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293048
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-293048

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Query Match	20.1%;	Score 406;	DB 8;	Length 1000;	
Best Local Similarity	70.7%;	Pred. No. 1.8e-90;			
Matches 621;	Conservative	0;	Mismatches 205;	Indels 52;	Gaps 4;
QY	1177	CCGAGCATGGCTTCCACGAGAGCTGCTCGCTCGGAGAGGAGTGTCTGCAAGACTTCCGA	1236		
Db	1	CCCAGCAAAAGCTTCCACGAGGAGCTCGCTTGGAGAGTACTTACTACAAAGACTGCGAG	60		
QY	1237	TCACACAGATGATGAGCTGTGGACGATGACAAACATGGGATCGCTATGGGCTGCCCC	1296		
Db	61	TCAGGCCAGTGTCTGCAGCTATGGGACGATG---ACTTGGAGCGCTATGGGCTGCCCC	117		
QY	1297	ATGGACAAGTACATCACAAGCGCTCGGCTCTAGTATGGCTGGCCTGCTACTCTTTGGCT	1356		
Db	118	ATGGACAAATACATCACAAGCGCTGGGCGCTCGTGTGCTGGCCTGCTACTCTTTGCT	177		
QY	1357	GGGGCGCTTTCTTCTCTCTCTTCTTCAAAAAGGACCGCAGGAAA-----	1401		
Db	178	GCTGCGCTTTCTCCTCATCTCTCTTCTCAAAAAGATCACGCGAAGGGTGGCTGAGGCTC	237		
QY	1402	-----GGGGCGCTGGCTCCGACAGCGCTTGTCTCTCCAC	1437		
Db	238	TTGAAACAGAGCTCGCTCGGGGGCGGCGCCACAGGGCGCGCGCTGTCTCTCTAC	297		
QY	1438	TCGCGCGAGGACGGGCTTACAGAGCTGTGTGGAGACACTGGCTCCGCTGTGAGCCAG	1497		
Db	298	TCAGCCGATGACTCGGGTTTCAGCGCCTGTGTGGCGCCTGGCTCGGCCCTGTGCCAG	357		
QY	1498	ATGCCACTGCGGCTGGCGCTGACTCTGTGGAGCGCCCGCGAGCTGAGCGCGCAGGAGCC	1557		
Db	358	CTGCGGCTGGCGTGGCCGTAGACTGTGGAGCGCTGTGAACTGAGCGCGCAGGGGCTC	417		

Qy	1558	CTAGCTGGTTCCACACACAGCGAGCGCGTATCTCGCAGGAGGGTGCGTGGTAACTCTT	16117
Db	418	GTGGCTTTGGTTTTCACGCGCAGCGCGCAGACCCCTGCAAGAGGCGCGTGGTGGTCTTG	477
Qy	1618	CTCTTTCGCCCGCGCGTGGCGCAGTGTGTCAGCAGTGGCTGTCAGCT-----CCAG	1668
Db	478	CTCTTCTCTCCCGTGGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGG	537
Qy	1669	ACAGTAGAGCCCGGCGCGCATGACGCCCTCTGCGCCCTGGCTCGCTGCTACCTCCGAT	1728
Db	538	CCCGGGGCGCAGCGCCCGCACGACGCCCTTCGCGCCCTCGTCACTGCTGCTGCCCGAC	597
Qy	1729	TTCTCTGCAAGCGCGGGCGACCGGCGGCTACGTGGGGTCTTACTTCGAGCGGCTGCTGCAC	1788
Db	598	TTCTTGCAGGGCCGGGGCGCCGGCAGCTACGTGGGGGGCCTGCTTCGACAGGCTGCTCCAC	657
Qy	1789	CCAGACTCTGTGCCCTCTCCCGTTCGCGGTGGCCCCGCTCTTCTCCCTGCCACGCGACGTG	1848
Db	658	CCGSAACCGGTACCCCGGCCCTTTTCCGCAACCGTGCCTGCTTCACACTGCCCTCCCAACTG	717
Qy	1849	CCGGCTTTCTGGATGCACTGCAAGGAGGCTGTCTCACTTCGCGGGGGCGACCCGCGGAC	1908
Db	718	CCAGACTCTCTGGGGGGCCCTGCACAGCCTCGCGCCCCCGGCTTCGCGGGCGGCTCCAGAG	777
Qy	1909	CGGGTGAAACGAGTGACCCAGGCGCTCGGGTCCGCTCCCTCGACAGCT-GTACTTCTAGCTC	1967
Db	778	AGACGGAGCAAGTGTCCCGGCCCTTCACCCAGCCCTGGATAGTACTTCCATCCCCCG	837
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RESULT 15

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RESULT 15
US-11-266-748A-344477/c
; Sequence 344477, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 344477
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-344477

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Query Match	20.1%	Score 406;	DB 8;	Length 1000;
Best Local Similarity	70.7%	Pred. NO. 1.8e-90;		
Matches 621;	Conservative	0;	Mismatches 205;	Indels 52;
				Gaps 4;

Search completed: August 17, 2006, 00:44:15
Job time : 720 secs

RESULT 2	AX360307	2256 bp	DNA	linear	PAT 13-FEB-2002
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LOCUS	AX360307				
DEFINITION	AX360307.1 GI:18675809				
ACCESSION					
VERSION					
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Gao, Z.				
AUTHORS	Murine cytokine receptor				
TITLE	Patent: WO 0204519-A 1 17-JAN-2002;				
JOURNAL	ZymoGenetics, Inc. (US)				
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Best Local Similarity	100.0%;	Pred. No. 0;			
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Qy	61	CTGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGCTCTCTAGGCCTCTCTCTGCCAC	120		
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Qy	121	CTCTGGGATGGTGACGTGCTCTGCTCTGCTGGAAAGCCTCCAGTCTGCCCAGGCCCTGTG	180		
Db	317	CTCTGGGATGGTGACGTGCTCTGCTCTGCTGGAAAGCCTCCAGTCTGCCCAGGCCCTGTG	376		
Qy	181	CTAGTGCTACCCCGCTCGACAGGACCTGGTGTCTGAGGTGTCCACAGAAGACAGATTGC	240		
Db	377	CTAGTGCTACCCCGCTCGACAGGACCTGGTGTCTGAGGTGTCCACAGAAGACAGATTGC	436		
Qy	241	GCCCTCCGTGTCCTGTGGTGGTCCACTTGGCCCTGTCATGGGCCTCGGGCAGAGCCTGAA	300		
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Qy	301	GAAGCTGGAAAGTCTGATTTCAGAACTCCAGAGTCTTAGAACGCTCTCTCCAGGCCACG	360		
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Qy	361	GTGTGTCTCTCTTCCAGGCCCTACCCCATCGCCCGCTGTGCCCTGTCTGGAGTTCAGGTG	420		
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2177 TGTACTTCTAGCTCGGAAGCCCGAGCTGCTGAGGAGTGGACCTGGGACCTTGCAC 2236
2014 ACCTAGAA 2022
2237 ACCTAGAA 2245

RESULT 4
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LOCUS CS251267 2287 bp DNA linear PAT 18-JAN-2006
DEFINITION Sequence 29 from Patent WO2005123778.
ACCESSION CS251267
VERSION CS251267.1 GI:85361025
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

AUTHORS Presnell, S.R.
TITLE Soluble zcytor14, anti-zcytor14 antibodies and binding partners and methods of using in inflammation
JOURNAL Patent: WO 2005123778-A 29 29-DEC-2005;
ZymoGenetics, Inc. (US)
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 3; Indels 45; Gaps 1;
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DB 257 CTGGAGAGACTGATGGAGCCTCAGGACACTGACAGCTGCTCTCTAGGCTCTCTCTGCCCAC 316
QY 121 CTCTGGAGTGTGAGCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 317 CTCTGGAGTGTGAGCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
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ACCESSION	AX360310.1		
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AUTHORS	Gao, Z.		
TITLE	Murine cytokine receptor		
JOURNAL	Patent: WO 0204519-A 4 17-JAN-2002;		
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Qy	61	CTGGAGAGACTGATGGAGCTCAGGACATGCACGTGCCTCTCTAGSGCCTCTCTCTGCGCAC	120
Db	257	CTGGAGAGACTGATGGAGCCTCAGGACATGCACGTGCCTCTCTAGSGCCTCTCTCTGCGCAC	316
Qy	121	CTCTGGGATGGTGACGTGCTCTGCTCGCTCGCTCGAAGCCTCCAGTGTGCCCCAGGCCCTGTG	180
Db	317	CTCTGGGATGGTGACGTGCTCTGCTCGCTCGCTCGAAGCCTCCAGTGTGCCCCAGGCCCTGTG	376
Qy	181	CTAGTGCTTACCCGCTGCAGACGGAGCTGGTGTCTAGAGTGTCCACAGAGA CAGATTGC	240
Db	377	CTAGTGCTTACCCGCTGCAGACGGAGCTGGTGTCTAGAGTGTCCACAGAGA CAGATTGC	436

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Qy |||||
1429 C T C C T C C A C T C C G C C A C G A G C G G G C T A C A G A C C T C T G T G G A G A C A C T G C G T C C G G 1488
Db |||||
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Qy |||||
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Db |||||
1757 T T G A C C A G A T G C C A C T G C G C T G G C C T G G A C C T G T G A G C C C G C G A G C T G A G C G G 1816
Qy |||||
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1817 C A C G A G C C C T A G C C T G T T C C A C C A C A G A C C C C G T A T C C T C A G A G A G G T G G C G T G 1876
Qy |||||
1609 G T A A T C C T T C T C T C C C C G C C G T G G C C A G T G T C A G A C T G G C T G C A G C T C C A G 1668
Db |||||
1877 G T A A T C C T T C T C T C C C C G C C G T G G C C A G T G T C A G A C T G G C T G C A G C T C C A G 1936
Qy |||||
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Db |||||
1937 A C A G T G A G C C C G C C C A T G A C C C C T C G C C C C T G C C C T G C C T G C T A C C C G A T 1996
Qy |||||
1729 T T C C T G C A A G C C G C G C A C C G C C T A C G T C G G G G T C T A C T C G A C G G G T G C T G C A C 1788
Db |||||
1997 T T C C T G C A A G C C G C G C A C C G C C C T A C G T C G G G G T C T A C T C G A C G G G T G C T G C A C 2056
Qy |||||
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Db |||||
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Qy |||||
1849 C G G C T T T C C T G A T G C A C T G C A G G A G C T C C A C T C C G C G G G C G A C C C C G G A C 1908
Db |||||
2117 C G G C T T T C C T G A T G C A C T G C A G G A G C T G C T C A C T T C C G C G G G C A C C C C G G A C 2176
Qy |||||
1909 C G G T G G A A C A G T G A C C C A G C C T G C G C T G C G C C C C T G G A C A G C T G A C T T C T A G C T G 1968
Db |||||
2177 C G G T G G A A C A G T G A C C C A G C C T G C G C T G C G C C C C T G G A C A G C T G A C T T C T A G C T G 2236
Qy |||||
1969 G A A G C C C A G C T G C T G A G A A T G G A C C C T G G A C C C T G C A C T A C A C T A G A A 2022
Db |||||
2237 G A A G C C C A G C T G C T G C A G A A T G G A C C C T G G A C C C T G C A C T A C A C T A G A A 2290

RESULT 6

CS135270
LOCUS 2314 bp DNA linear PAT 09-AUG-2005
DEFINITION Sequence 7 from Patent WO2005065711.
ACCESSION CS135270
VERSION CS135270.1 GI:72067721
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1
REFERENCE Gorman,D.M.
AUTHORS Mammalian receptor proteins; related reagents and methods
TITLE Patent: WO 2005065711-A 7 21-JUL-2005;
JOURNAL Schering Corporation (US)
FEATURES Location/Qualifiers
source 1..2314
/organism="Mus musculus"
/mol_type="unassigned DNA"

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1849 CCGGCTTTCTCGATGCACTGCAGGAGGCTGCTCCACTTCCGCGGGGCGACCCGCGGAC 1908
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1969 GAAGCCCCAGGCTCTCGAGGAATGGACCTGGGACCTGGCACTACACTAGAA 2022
2239 GAAGCCCCAGGCTCTCGAGGAATGGGACCTGGGACCTGGCACTACACTAGAA 2292

RESULT 7
AX350976 2314 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 10 from Patent WO0190358.
ACCESSION AX350976
VERSION AX350976.1 GI:18616352
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1
Gorman, D. M.
Mammalian receptor proteins: related reagents and methods
Patent: WO 0190358-A 10 29-NOV-2001;
SCHERING CORPORATION (US)
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mat_peptide
ORIGIN

Query Match 95.6%; Score 1933.6; DB 2; Length 2314;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 2018; Conservative 0; Mismatches 4; Indels 72; Gaps 1;

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Db 199 ATGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
Qy 61 CTGAGAGACTGTAGGAGCTCAGGACACTGCACGCTGCTCTTAGCGCTCTCCTGCCAC 120

259 CTGAGAGACTGTAGGAGCTCAGGACACTGCACGCTGCTCTTAGGCGCTCTCCTGCCAC 318
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319 CTCTCGGATGGTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
181 CTAGTGCCTTACCCGCTTCAGACGAGCTGTGTGAGGTGTCCACAGAAACAGATTCG 240
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421 CCGCTGACCTGGTGCAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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481 GCTAGTCTTTGGGCTGAGGTACAGATCTGCTTACACGAGCCAGGTTACCAGAAAGAG 540
679 GCTAGTCTTTGGGCTGAGGTACAGATCTGCTTACACGAGCCAGGTTACCAGAAAGAG 738
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739 CTCAACCTCACAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
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799 AGCTGCTGGTCTCTGCTGCTCAATGTGTCTACAGATGGTGACAATGCTCTCTGACA 858
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859 CTGGATGCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGTGCTGCTGCTGCTGCTGCTG 918
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919 GCTCTCAATCTCTGTGTGCTCAAAAACCTGACTGCAACCTCAGAAATTAATTTAAACCA 978
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979 ACAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
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Qy 1309 ATCCACAGCGCTGGGTCTAGTATGGCTGGCTGCTACTCTTGGCTGGCGCTTTTC 1368
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Db 1999 TTCTTCAAGCGCGCGGACCGGCGCTGCTGCGGCTTACTTTCAGCGGCTGTGTCAC 2058
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Qy 1909 CCGGTGGAACGAGTGAACCCAGGCGTGGCTGCGGCTGGACAGCTGTACTTCTAGCTG 1968
Db 2179 CCGGTGGAACGAGTGAACCCAGGCGTGGCTGCGGCTGGACAGCTGTACTTCTAGCTG 2238
Qy 1969 GAAGCCCCAGGCTGCTGCGAGGAATGGACCTGGGACCTGCACCTACACTAGAA 2022
Db 2239 GAAGCCCCAGGCTGCTGCGAGGAATGGACCTGGGACCTGCACCTACACTAGAA 2292

RESULT 9
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LOCUS AX360309 2022 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0204519.
ACCESSION AX360309
VERSION AX360309.1 GI:18675811
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Gao, Z.
TITLE Murine cytokine receptor
JOURNAL Patent: WO 0204519-A 3 17-JAN-2002;
ZymoGenetics, Inc. (US)
LOCATION/Qualifiers
FEATURES
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Query Match 69.8%; Score 1412.2; DB 2; Length 2022;
Best Local Similarity 56.2%; Pred. No. 0;
Matches 1137; Conservative 464; Mismatches 421; Indels 0; Gaps 0;

Qy 1 ATGCCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 ATGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 61 CTGGAGAGACTGATGGAGCCCTCAGGACACTGACGACCTGCTCTCTAGGCTCTCTCTGCCAC 120
Db 61 YTNAGRMGNNTNATGGARCCNCARGAYACNCGNMGNTGYWSNYTNGNNTYWSNYTNGY 120
Qy 121 CTCTGGGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 YTNAGGAGGNGAYGTNTYTNCTGNGNWSNYTNCARWSNCGNNGNCGNCTG 180
Qy 181 TAGTGCTCTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 YTNCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 241 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 301 GAAGCTGGAAGTCTGATTCAGAACTCCAGAGTCTAGGAGCCCTCTCTCCAGGCCCGAC 360
Db 301 GARGCNGGNAARWSNGAYWSNGARYTNCARGARWSNMGNAAYGNCNWSNYTNCARGCNCAR 360
Qy 361 GTGGTGTCTCTCTCCAGGCTTACCCCATCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 GTNGTNTYWSNTTYCARGCNTAYCCNATHGNCNMGNTGYGCTGCTGCTGCTGCTGCTGCT 420
Qy 421 CCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 CCGCNGAYTNGTNCARCCNCGNNGNWSNMGNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

	Query Match	66.3%	Score 1341.2	DB 6	Length 2015
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					Gaps 2
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Db	177	ATGCGTGTCTCGTGGTTCCTGCTGTCCTTGGCACTGGGCGGAAACCTGTGGTGGTCTCT	236		
Qy	61	CTGGAGAGACTGATGGAGCCTCAGGACATGCACGCTGCTCTTAGGCCCTCTCCTGGCCAC	120		
Db	237	CTGGAGAGACTGATGGAGCCTCAGGACATGCACGCTGCTCTTAGGCCCTCTCCTGGCCAC	296		

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Db		1174	C T C G A G T T C C A T T G C T G T A A A G G C C A C C C T A A C C C T C T G T G T T C A G S T G A A C A C G C T G G A G	1233
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Db		1234	A A G C T G A G C T G C A G G A G T C T T G T G G G C T G A C T C C T C G G G G C C T C T C A A A G A C G A T G T G	1293
Qy		1102	C T G T T A G T G G A G A T G A A A C C G G C C T C A A C A A C A C A T C A G T C T G T G C T T T G G A A C C C A G T	1161
Db		1294	C T A C T G T T G G A G A C A C A G A G C C C C A G G A C A A C A G A T C C C T C T G T G C T T T G G A A C C C A G T	1353
Qy		1162	G G C T G T A C A C A C T G C C C A G C A T G G C C T C A C A G A G C T G C T C G C C T G G G A G A G G A G T T G	1221
Db		1354	G G C T G T A C T T C A C T A C C A G C A A A G C C T C C A C A G G G C A G C T C G C C T T G G A G A G T A C T T A	1413
Qy		1222	C T G C A A G A C T T C C G A T C A C A C C A G T G T A T G C A G C T G T G A A C A G A T G A C A A C A T G G A T C G	1281
Db		1414	C T A A G A C C T G C A G T C A G G C C A G T G T C T G A G C T A T G G A C G A T G - - A C T T G G A G A G C	1470
Qy		1282	C T A T G G C C T G C C C A T G A C A A G T A C A T C C A C A G G C G T G G G T C T A G T A T G C T G C C G C	1341
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Qy		1693	G C C C T C G C C C C T G G C T C A G C T C G T C T A C C C G A T T T C C T G C A A G C C C G G G C G A C C G C C	1752
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Qy		1753	C G C T A C C T C G G G T C T A C T T C G A C G G C T G C T G C A C C C A G A C T C T G F G C C C T C C C G T T C	1812
Db		1951	A G C T A C T G G G G C C T G C T T C G A C A G C T C T C A C C C G G A C C G C T A C C C G C C C T T T T C	2010
Qy		1813	G G C G T C G C C C G C T C T C C C T G C C C A C A G A G C T G C C G C C T T C C T G A T G A C A C T G C A G	1872
Db		2011	C G A C C G T G C C C G C T T C A C A C T G C C C C T C C A A C T G C C A G A C T T C C T G G G G C C C T G C A G	2070
Qy		1873	G A G G C T G C T C C A C T T C C G C G G G C G A C C C G C G A C C G G G T G G A A C A G A T G A C C A G G C G C	1932
Db		2071	C A G C C T C G C C C G C G T T C G G G C G G C T C A A G A G A G A C G G A G C A A G T G T C C C G G C C	2130
Qy		1933	C T C G G T C C C C C T G G A C A C T - G T A C T T C T A G C T C G G A A G C C C A G C C A G G C T G C T G C A G G A	1991
Db		2131	C T T C A G C A C C C C T G G A T A G T A C T T C C A T C C C C C G G G A C T C C C G C C C G G A C G C G G G	2190
Qy		1992	A T G G A C C T G G G A C	2005
Db		2191	G T G G A C C A G G G G C	2204

[illegible]

Fri Aug 18 07:16:36 2006

QY	1102	CTGTTAGTGGAGTGAATAACCGGCTCTCAACACACATCAGTCTGTGTGCTTTGGAAACCCAGT	1161
DB	1373	CTACTGTTGGAGACACGAGGCCCCCAGGACACAGATCCCTCTGTGCTTTGGAAACCCAGT	1432
QY	1162	GGCTGTACACCACTGCCACAGCATGGCTTCCAGGAGAGTGTCTCCCTTGGGAGGAGGAGTTG	1221
DB	1433	GGCTGTACTTCACTACCCAGCAAAAGCCTCCAGGAGGAGTCCGCTTGGAGAGTACTTAA	1492
QY	1222	CTGCAAGACTTCGATGATCACACAGTGTATGACAGTGTGTGAACAGATGACAAATGGGATCG	1281
DB	1493	CTACAAGACTTCAGTTCAGGCTAGTGTCTGACAGTATGGACGATG---ACTTGGGAGCG	1549
QY	1282	CTATGGGCTTGGCCCATGGACAAGTATCATCCAGGCGCTGGGTCTTAGTATGCTGTGCC	1341
DB	1550	CTATGGGCTTGGCCCATGGACAATATACATCAACAGCGCTGGGCGCTCTGTGTGCTGTGCC	1609
QY	1342	TGCCTACTCTTGGCTGGGCGCTTTTCTTCTTCTCTTCTTAAAGAGACCGCAGGAAA	1401
DB	1610	TGCCTACTCTTGGCGCTGGCGTTTCCCTCATCTCTCTTCTCAAAAAGATCAACGANA	1669
QY	1402	-----GCGGCGCGCTGGCTTCGCGACG	1422
DB	1670	GGGTGGCTGAGGCTTTGAAACAGGACGTCGCTCGGGGCGCGCCAGGGCGCGCGCG	1729
QY	1423	GCCTTGCTCTCCATCTCGCGCAGGAGCGGGTTACGAGCTGTGGTGGGAGCACTGGCG	1482
DB	1730	GCTCTGCTCTTACTACTCAGCCGATGACTCTGGGTTCGAGCGCTGTGGGCGCGCTGGCG	1789
QY	1483	TCCGGTGTAGCAGATGCCACTTCGGCTGGCGTGGACCTGTGGAGCGCGCGCAGCTG	1542
DB	1790	TGGGCGCTGTGCAGCTGCCCTCGCGTGGCGGTAGACCTGTGAGACCGTCTGTAACCTG	1849
QY	1543	AGCGCGCAGGAGCCCTAGCTGTGTCCACACACAGCGACCGCGTATCTCTGACGAGGGT	1602
DB	1850	AGCGCGCAGGGGCCCTGGCTTGGTTTACCGCGCAGCGCGCCAGACCCCTGCAGGAGGCG	1909
QY	1603	GGCGTGTAACTCTTCTTTCGCGCGCGCGCTGGCGCAGTGTGACGAGTGGCTGCA-	1661
DB	1910	GGCGTGGTGTCTGCTCTTCTCTCCCGTGGCTGGCTGTGCACGAGTGGCTACAG	1969
QY	1662	-----GCTCCAGACAGTGGAGCCGGGCGGATGACGCCCTCGCGCGCTGGCTCAGC	1713
DB	1970	GATGGGTGTTCGGGCGCGGGCGCACGGCCCGGCGACGTAAGTGGGGGCTGCTTC	2089
QY	1714	TGCGTGTACCCGATTTCTTGCAAGCGCGGCGCACCGCGCTACGTGCGGGGTCTACTTC	1773
DB	2030	TGCGTGTGCCGACTTCTTGACGGCGCGGCGCGCGACGTAAGTGGGGGCTGCTTC	2089
QY	1774	GACGGGTGTGCCACCACTGTGTGCCCTCCCGTTCGCGTCCGCGTCCGCTCTTCTTC	1833
DB	2090	GACAGGTGTCTCACCGCGACCGGTACCCGCGCTTTTCCGACGCGTGGGGGCTGCTTC	2149
QY	1834	CTGCCACGAGCTGCGCGCTTCTCTGGATGACATGACAGGAGGCTGTCTCACTTCCGCG	1893
DB	2150	CTGCCCTTCCCACTTGCCAGACTTCTTGGGGGCGCTTGCAGAGCTTCCGCGCCCGCTTC	2209
QY	1894	GGGCGACCGCGGACCGGGTGGAAACAGTGAACAGGCGCTCGGTTCGCGCTCGACAGC	1953
DB	2210	GGGCGGTCCAAAGAGAGCGGAGCAAGTGTCCCGGGCGCTTACGCCAGCCCTGGATAGC	2269
QY	1954	T-GTACTTCTAGCTCGGAAGCCCGGCTGCTCGAGGAATGGGACCTGGGAC	2005
DB	2270	TACTTCCATCCCCGGGGAATCCCGCGCGGAGCGCGGGTGGACACAGGCGC	2322

Search completed: August 17, 2006, 00:32:23
Job time : 11541 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 20:57:35 ; Search time 1330 Seconds
(without alignments)
10599.915 Million cell updates/sec

Title: US-10-719-202-1_COPY_197_2218
Perfect score: 2022
Sequence: 1 atgcctgtctcgtctct.....gacctgcactacactagaa 2022

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB	ID	Description
1	2022	100.0	2256	6	Aad24220 Murine cy
2	1980.2	97.9	2269	15	Aef05372 Mouse zcy
3	1962.2	97.0	2287	15	Aef05376 Mouse zcy
4	1940	95.9	2328	6	Aad24222 Murine cy
5	1933.6	95.6	2128	6	Ab134982 Murine cd
6	1933.6	95.6	2314	6	Aas18132 Mouse DNA
7	1933.6	95.6	2314	14	Aeb55651 Mouse DCS
8	1929.6	95.4	2331	6	Abk86568 Mouse inc
9	1412.2	69.8	2022	6	Aad24221 Murine cy
10	1330.2	65.8	2094	6	Aad24223 Murine Zc
11	1327.6	65.7	2094	4	Aas18133 Mouse DCR
12	1162.4	57.5	2255	4	Aac85027 Human cyt
13	1162.4	57.5	2255	10	Aad47894 Human cyt
14	1162.4	57.5	2255	15	Aef05348 Human ILI
15	1113.4	55.1	2380	4	Aas46223 Human DNA
16	1113.4	55.1	2380	4	Aaf92138 Human PRO
17	1113.4	55.1	2380	4	Aas09515 Human cdn
18	1113.4	55.1	2380	6	Ab574458 Human cdn

19	1113.4	55.1	2380	6	ABL88253	Human PRO
20	1113.4	55.1	2380	6	ABL95742	Human ang
21	1113.4	55.1	2380	8	ACA89673	cDNA enco
22	1113.4	55.1	2380	8	ACA73683	Human sec
23	1113.4	55.1	2380	8	ACA05998	Human sec
24	1113.4	55.1	2380	8	ACA66832	CDNA enco
25	1113.4	55.1	2380	8	ACA91244	Novel hum
26	1113.4	55.1	2380	8	ACD81621	Human cdn
27	1113.4	55.1	2380	8	ACF20407	Human sec
28	1113.4	55.1	2380	8	ACF19793	Human sec
29	1113.4	55.1	2380	8	ACD22081	Human sec
30	1113.4	55.1	2380	8	ACF13246	Human sec
31	1113.4	55.1	2380	8	ACD25349	Human sec
32	1113.4	55.1	2380	8	ACF00398	Human sec
33	1113.4	55.1	2380	8	ACA60443	Novel hum
34	1113.4	55.1	2380	8	ACA72455	Novel hum
35	1113.4	55.1	2380	8	ACD04979	Novel hum
36	1113.4	55.1	2380	8	ACD18440	Human sec
37	1113.4	55.1	2380	8	ACD08447	Human sec
38	1113.4	55.1	2380	8	ACA88881	Novel hum
39	1113.4	55.1	2380	8	ACA70323	Human sec
40	1113.4	55.1	2380	8	ACD12545	Novel hum
41	1113.4	55.1	2380	8	ACC74460	Human sec
42	1113.4	55.1	2380	8	ACD16088	Human sec
43	1113.4	55.1	2380	8	ACD25656	Novel hum
44	1113.4	55.1	2380	8	ACD18133	Human sec
45	1113.4	55.1	2380	8	ACC88420	Human sec

ALIGNMENTS

RESULT 1	
AAD24220	
ID	AAD24220 standard; DNA; 2256 BP.
XX	
AC	AAD24220;
XX	
DT	17-MAY-2002 (first entry)
XX	
DE	Murine cytokine receptor Zcytor14 DNA.
XX	
KW	Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW	gene therapy; protein therapy; gene; ds.
XX	
OS	Mus sp.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	197..2221
FT	/*tag= a
FT	/product= "Cytokine receptor, Zcytor14"
FT	197..256
FT	/*tag= b
FT	257..2218
FT	/*tag= c
FT	/product= "Mature cytokine receptor, Zcytor14"
XX	
PN	WO200204519-A2.
XX	
PD	17-JAN-2002.
XX	
PF	05-JUL-2001; 2001WO-US021344.
XX	
PR	06-JUL-2000; 2000US-0216446P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Gao Z;
XX	
DR	WPI; 2002-179701/23.
XX	
DR	P-PSDB; AAE14559.
XX	
PT	New murine cytokine receptor, Zcytor14, and polynucleotides encoding the

Db	1937	CGGGCGGACCGGCGCGCTACGTGGGGTCTACTTCGACGGGCTGCTGCACCCGAGACTCTGTG	1996		
Qy	1801	CCCTCCCGCTTCGCGCTCGCCCGCTCTTCTCCCTGCCACGACGCTGCCGGCTTTTCCCTG	1860		
Db	1997	CCCTCCCGCTTCGCGCTCGCCCGCTCTTCTCCCTGCCACGACGCTGCCGGCTTTTCCCTG	2056		
Qy	1861	GATGCACCTGACGGAGGCTGCTCCACTTCGCGGGGCGACCCGCGGACCGGGTGGAAACGA	1920		
Db	2057	GATGCACCTGACGGAGGCTGCTCCACTTCGCGGGGCGACCCGCGGACCGGGTGGAAACGA	2116		
Qy	1921	GTGACCCAGGCGCTGCGGCTCGCCCTCGACAGCTGTACTTCTAGCTCGGAAGGCCAGGC	1980		
Db	2117	GTGACCCAGGCGCTGCGGCTCGCCCTCGACAGCTGTACTTCTAGCTCGGAAGGCCAGGC	2176		
Qy	1981	TGCTGCGAGGAAATGGGACCTGGGACCTGGCACTACACTAGAA	2022		
Db	2177	TGCTGCGAGGAAATGGGACCTGGGACCTGGCACTACACTAGAA	2218		
RESULT 2					
AEF05372					
ID	AEF05372 standard; cDNA; 2269 BP.				
XX	AC				
XX	AC				
XX					
DT	23-FEB-2006 (first entry)				
XX					
DE	Mouse zcytoR14 variant cDNA SEQ ID NO 25.				
XX					
KW	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;				
KW	antiarthritic; dermatological; antipsoriatic; antibacterial;				
KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;				
KW	inflammatory bowel disease; asthma; respiratory disease;				
KW	ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;				
KW	gastrointestinal disease; arthritis; antiarthritic;				
KW	musculoskeletal disease; psoriasis; antipsoriatic;				
KW	dermatological disease; immune disorder; atopic dermatitis;				
KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;				
KW	antibacterial; immunosuppressive; infection; zcytoR14; mutant;				
XX	coding sequence; ss.				
XX					
OS	Mus musculus.				
XX					
XX					
FH	Key Location/Qualifiers				
FT	197..2248				
PT	/*tag= a				
FT	/product= "Mouse zcytoR14 variant "				
FT					
XX	WO2005123778-A2.				
PN					
XX					
XX	29-DEC-2005.				
PD					
XX					
XX	10-JUN-2005; 2005WO-US020521.				
PP					
XX					
XX	10-JUN-2004; 2004US-0578805P.				
PR					
XX					
PA	(ZYMO) ZYMOGENETICS INC.				
XX					
PI	Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;				
PI	Jaspers SR, Billsborough J;				
PI					
XX					
XX	WPI; 2006-067457/07.				
DR	P-PSDB; AEF05373.				
DR					
XX					
PT	New isolated soluble receptor comprises at least one ZcytoR14 subunit,				
PT	useful for treating an inflammatory disease, e.g. asthma, inflammatory				
PT	bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or				
PT	psoriasis.				
XX					
PS	Example 28; SEQ ID NO 25; 205pp; English.				
XX					
CC	The invention describes an isolated soluble receptor comprises at least				

	CC	one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
	CC	comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
	CC	amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
	CC	ID NO. 24) given in the specification. Also described are: an isolated
	CC	soluble receptor comprising Zcytor14, where Zcytor14 comprises a
	CC	polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
	CC	the pro-inflammatory activity of either IL-17A comprising fully defined
	CC	155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
	CC	amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
	CC	to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
	CC	and where the antibody or antibody fragment reduces the pro-inflammatory
	CC	activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
	CC	reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
	CC	afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
	CC	role; and treating a pathological condition in a subject associated with
	CC	Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
	CC	subunit is useful for treating an inflammatory disease, e.g. asthma;
	CC	chronic inflammatory disease selected from inflammatory bowel disease,
	CC	ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
	CC	psoriasis; or acute inflammatory disease selected from endotoxemia,
	CC	septicemia, toxic shock syndrome, or infectious disease. This sequence
	CC	represents a mouse IL-17A and IL-17F receptor zcytor14 variant.
	XX	
	QQ	Sequence 2269 BP; 405 A; 713 C; 685 G; 466 T; 0 U; 0 Other;
		Query Match 97.9%; Score 1980.2; DB 15; Length 2269;
		Best Local Similarity 98.5%; Pred. No. 0;
		Matches 2019; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
QY	1	ATGCCTGTGTCCTGGTTCCTGCTCCTCGGCACTGGGCCGAACCCCTGTGCTCTCT 60
DB	197	ATGCCCTGTGCTCCTGGTTCTGCTGTGCTTGCGACTGGGCCGAACCCCTGTGCTCT 256
QY	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGTCTCTAGGCGCTCTCTGCCAC 120
DB	257	CTGGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGTCTCTAGGCGCTCTCTGCCAC 316
QY	121	CTCTGGAGTGGTAGCGTGTCTCTGCTGCTCTGGAAAGCTTCAGTCTGCCAGGCCCTGTG 180
DB	317	CTCTGGAGTGGTAGCGTGTCTGCTCTGCTCTGGAAAGCCTTCAGTCTGCCAGGCCCTGTG 376
QY	181	CTAGTGCTCTACC CGCTGCAGACGGAGCTGGTCTCAGAGTGTCCACAGAAGACAGATTGC 240
DB	377	CTAGTGCTCTACC CGCTGCAGACGGAGCTGGTGTCTGAGGTGTCCACAGAAGACAGATTGC 436
QY	241	GCCTCCCGTGTCCGTGTGTGGTGGTCCAATTGGCCGTGCATGGGCACCTGGGCAGAGCTGAA 300
DB	437	GCCTCTGTGTCTGTGGTGGTGGTCCAATTGGCCGTGCATGGGCACCTGGGCAGAGCTGAA 496
QY	301	GAGCTGGAAAGTCTGATTCAGAACTCCAGAGTCTAGGAAAGCCTCTCTCCAGGCCCCAG 360
DB	497	GAGCTGGAAAGTCTGATTCAGAACTCCAGAGTCTAGGAAAGCCTCTCTCCAGGCCCCAG 556
QY	361	GTGGTGCTCTCTCTTCAGAGGCTACCCCATCGCCCGCTGTGCTCCCTGTGGAGGTCCAGGTG 420
DB	557	GTGGTGCTCTCTCTTCAGAGGCTACCCCATCGCCCGCTGTGCTCCCTGTGGAGGTCCAGGTG 616
QY	421	CCCCTGACCTGTGTGAGCGCTGTGTGAGTCCGTTGGGTTCCTGCGGTATTTGACTGTTTCGAG 480
DB	617	CCCCTGACCTGTGTGAGCGCTGTGTGAGTCCGTTGGGTTCCTGCGGTATTTGACTGTTTCGAG 676
QY	481	GCTAGTCTTTGGGGCTCAGGTACAGATCTGGTCTTCTCACAGAACCCAGGTACCAAGAAGAG 540
DB	677	GCTAGTCTTTGGGGCTCAGGTACAGATCTGGTCTTCTCACAGAACCCAGGTACCAAGAAGAG 736
QY	541	CTCAACCTCTCACAGCAGCTGCCT-----GATGCTGAC 573
DB	737	CTCAACCTCTCACAGCAGCTGCCTGCTCCTGCCCTGCTCAATGTGTCTACAGATGCTGAC 796
QY	574	AATGTCTTCTTGACA CTAGATGTCTCTGAGAGCAGGACTTTAGCTTCTTACTGTACTCTG 633
DB	797	AATGTCTTCTTGACA CTAGATGTCTCTGAGAGCAGGACTTTAGCTTCTTACTGTACTCTG 856

CC The invention describes an isolated soluble receptor comprises at least

[illegible]

Db	1937	TGCGTGTACCCGATTCTCTGCAAGCCGGCGGACCGGCCGTACGTTCGGGGTCTACTTC	1996
QY	1774	GACGGGCTGTGCACCAGACTCTGTGCCCTCCCGTTCCGGGTCCGCCCGCGTCTTCTC	1833
Db	1997	GACGGGCTGTGCACCAGACTCTGTGCCCTCCCGTTCCGGGTCCGCCCGCGTCTTCTC	2056
QY	1834	CTGCCCACGCAGCTGCCGCTTTCTTGATGCACTGCAGGGAGGCTGTCCACTTCGGCG	1893
Db	2057	CTGCCCTCGAGTCCGGCTTTCTTGAATGCACTGCAGGGAGGCTGTCCACTTCGGCG	2116
QY	1894	GCGCGAACCCGCGGACCGGGTGGAAACGAGTGACCCAGCGCTCGCGTCCGCCCTGGACAGC	1953
Db	2117	GCGCGAACCCGCGGACCGGGTGGAAACGAGTGACCCAGCGCTCGCGTCCGCCCTGGACAGC	2176
QY	1954	TGTACTTCTTAGTTCGGAAGCCCCAGGCTGTCTCGAGGAATGGGACCTGGGACCTGCAC	2013
Db	2177	TGTACTTCTTAGTTCGGAAGCCCCAGGCTGTCTCGAGGAATGGGACCTGGGACCTGCAC	2236
QY	2014	ACACTAGAA	2022
Db	2237	ACACTAGAA	2245
<hr/>			
RESULT 3			
AEF05376 standard; cDNA; 2287 BP.			
XX	ID	AEF05376	
XX	AC	AEF05376;	
XX	DT	23-FEB-2006	(first entry)
XX	DE	Mouse zcytoR14 variant CDNA SEQ ID NO 29.	
XX	KW	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;	
XX	KW	antiarthritic; dermatological; antipseudotubercular; antibacterial;	
XX	KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;	
XX	KW	inflammatory bowel disease; asthma; respiratory disease;	
XX	KW	ulcerative colitis; antiulcer; Crohn's disease; gastrointestinal-gen.;	
XX	KW	gastrointestinal disease; arthritis; antiarthritic;	
XX	KW	musculoskeletal disease; psoriasis; antipsoriatic;	
XX	KW	dermatological disease; immune disorder; atopic dermatitis;	
XX	KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;	
XX	KW	antibacterial; immunosuppressive; infection; zcytoR14; mutant;	
XX	KW	coding sequence; ss.	
XX	OS	Mus musculus.	
XX	FH	Key	Location/Qualifiers
FT	CDS	197..2266	
FT		/tag= a	
FT		/product= "Mouse zcytoR14 variant"	
XX	PB	WO2005123778-A2.	
XX	PD	29-DEC-2005.	
XX	PF	10-JUN-2005; 2005WO-US020521.	
XX	PR	10-JUN-2004; 2004US-0578805P.	
XX	PA	(ZYMO) ZYMOGENETICS INC.	
XX	PI	Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;	
PI	PI	Jaspers SR, Billsborough J;	
XX	PI	WPI; 2006-067457/07.	
DR	DR	P-PSDB; AEF05377.	
XX	PT	New isolated soluble receptor comprises at least one zcytoR14 subunit,	
PT	PT	useful for treating an inflammatory disease, e.g. asthma, inflammatory	
PT	PT	bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or	
PT	PT	psoriasis.	

[illegible]

|||||
Db 1877 GTGGGCGAGTGTGACAGTGGCTGAGCTCCAGACAGTGGAGCCGGGCGCATGACGCC 1936
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Qy 1696 CTCGCGCGCTGGCTCAGCTGGTGTCTACCGATTCTGCAAGCCGGGCGAGCCGGCCGC 1755
|||||
Db 1937 CTCGCGCGCTGGCTCAGCTGGTGTCTACCGATTCTGCAAGCCGGGCGAGCCGGCCGC 1996
|||||
Qy 1756 TACGTCGGGGTCTACTTCGACGGGCTGTGCAACCAGACTGTGTCCTCCCGTTCCGC 1815
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Db 1997 TACGTCGGGGTCTACTTCGACGGGCTGTGCAACCAGACTGTGTCCTCCCGTTCCGC 2056
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Qy 1816 GTGCGCCCGCTCTTCTCCCTGCCCCACGAGCTGCGCGTTTCTGATGACATCCAGGA 1875
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Qy 1876 GGCTGCTCAGCTTCGCGGGGGGACCCCGGACCGGGTGGAAACGAGTGACCCAGCGCTG 1935
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Db 2117 GGCTGCTCAGCTTCGCGGGGGGACCCCGGACCGGGTGGAAACGAGTGACCCAGCGCTG 2176
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Qy 1936 CGGTCCGCGCTGACAGCTGTACTTCTAGCTCGGAAGCCCGAGGCTGTGCGAGGAATGG 1995
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Db 2177 CGGTCCGCGCTGACAGCTGTACTTCTAGCTCGGAAGCCCGAGGCTGTGCGAGGAATGG 2236
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Qy 1996 GACCTGGGACCTGCACTACATAGAA 2022
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Db 2237 GACCTGGGACCTGCACTACATAGAA 2263
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RESULT 4
ID AAD24222 standard; DNA; 2328 BP.
XX
AC AAD24222;
XX
DT 17-MAY-2002 (first entry)
XX
DE Murine cytokine receptor Zcytor14 variant, Zcytor14-1 DNA.
DE
KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW gene therapy; protein therapy; Zcytor14-1; gene; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 197..2293
CDS /*tag= a
FT /*product= "Cytokine receptor Zcytor14 variant, Zcytor14-1"
FT
XX
XX WO200204519-A2.
XX
XX 17-JAN-2002.
XX
XX 05-JUL-2001; 2001WO-US021344.
XX
XX 06-JUL-2000; 2000US-0216446P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z;
XX
XX WPI; 2002-179701/23.
XX P-ESDB; AAE14560.
XX
XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
XX receptor, useful for treating inflammation, specifically rheumatoid
XX arthritis, and as educational tools or in research.
XX
XX Claim 8; Page 92-95; 99pp; English.
XX
XX The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
XX polypeptide is useful for identifying or isolating Zcytor14 ligands, in
XX preparing antibodies, in identifying proteins or peptide cleavage sites,
XX

in amino acid sequence analysis, and in monitoring biological activities
of both the native and tagged protein in vitro or in vivo. Polypeptides
having Zcytor14 activity can be used to treat inflammation, such as
rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational
tool in genetics, molecular biology, protein chemistry and antibody
production analysis, in the preparation of expression constructs for
bacterial, viral or mammalian expression, in determining mRNA and DNA
localisation of Zcytor14 polynucleotide in tissues, for identifying
related polynucleotides and polypeptides by nucleic acid hybridisation,
in linkage-based testing for various diseases in murine models, and to
determine whether a subject's chromosomes contain a mutation in the
Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo
diagnosis, and for detecting and localising Zcytor14 gene expression in
tissue samples. The present sequence is murine Zcytor14 variant, Zcytor14
-1 DNA
XX
SQ Sequence 2328 BP; 429 A; 726 C; 702 G; 471 T; 0 U; 0 Other;
Query Match 95.9%; Score 1940; DB 6; Length 2328;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 0; Indels 72; Gaps 1;
Qy 1 ATGCTGTGTCCTGGTTCCTGCTGCTGCTGGCACTGGCGCAACCTGTGGTGTCTCT 60
Db 197 ATGCTGTGTCCTGGTTCCTGCTGCTGCTGGCACTGGCGCAACCTGTGGTGTCTCT 256
|||||
Qy 61 CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTGTCTCTAGGCTCTCTCTGCCAC 120
Db 257 CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTGTCTCTAGGCTCTCTCTGCCAC 316
|||||
Qy 121 CTCTGGGATGGTGAAGTGTCTGCTGCTGCTGGAGAGCTGCTGCTGCTGCTGCTGCTG 180
Db 317 CTCTGGGATGGTGAAGTGTCTGCTGCTGCTGGAGAGCTGCTGCTGCTGCTGCTGCTG 376
|||||
Qy 181 CTAGTGTCTACCCGCTGACGAGCGAGCTGTGTGTGAGGTGTCCACAGAGACAGATTCG 240
Db 377 CTAGTGTCTACCCGCTGACGAGCGAGCTGTGTGTGAGGTGTCCACAGAGACAGATTCG 436
|||||
Qy 241 GCCCTCCGTCCTGTCGTGGTGTCCACTTGGCCGCTGATGGGCACTGGGCGAGCCCTGAA 300
Db 437 GCCCTCCGTCCTGTCGTGGTGTCCACTTGGCCGCTGATGGGCACTGGGCGAGCCCTGAA 496
|||||
Qy 301 GAAGCTGGAAAGTCTGATTCAGAACTCCAGGAGCTAGGACGCTCTCTCCAGGCCCGAG 360
Db 497 GAAGCTGGAAAGTCTGATTCAGAACTCCAGGAGCTAGGACGCTCTCTCCAGGCCCGAG 556
|||||
Qy 361 GTGGTGTCTCTCTCCAGGCCCTACCCCATCCCGCTGTGCTGCTGAGGTTCAGGTG 420
Db 557 GTGGTGTCTCTCTCCAGGCCCTACCCCATCCCGCTGTGCTGCTGAGGTTCAGGTG 616
|||||
Qy 421 CCCGCTGACCTGGTGCAGCTGGTGCAGTCCGTGGGTTCTGGGTATTTGACTGTTTCGAG 480
Db 617 CCCGCTGACCTGGTGCAGCTGGTGCAGTCCGTGGGTTCTGGGTATTTGACTGTTTCGAG 676
|||||
Qy 481 GCTAGTCTGGGGCTGAGGTACAGATCTGGTCTTCTACAGAAAGCCAGGTACAGAAAGAG 540
Db 677 GCTAGTCTGGGGCTGAGGTACAGATCTGGTCTTCTACAGAAAGCCAGGTACAGAAAGAG 736
|||||
Qy 541 CTCACCTCACAAGCAGCTGCCT----- 564
Db 737 CTCACCTCACAAGCAGCTGCCTGCTGAGGGGTCTTGAAGTCCGGGACAGCATCCAG 796
|||||
Qy 565 -----GATGGTGACAATGCTCTCTTGACA 588
Db 797 AGCTGCTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 856
|||||
Qy 589 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGCTGCTGCTGCTGCTGCTGCTG 648
Db 857 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGCTGCTGCTGCTGCTGCTGCTG 916
|||||
Qy 649 GCTCTCAAAATCCTTGTGTACAAAAACCTGACCTGGACCTCAGAACTATTACTTTAAACCCAC 708
Db 917 GCTCTCAAAATCCTTGTGTGTACAAAAACCTGACCTGGACCTCAGAACTATTACTTTAAACCCAC 976

709 ACAGACCTGGTTCCCTGCTCTGCAATTCAGGTGTGGTGGCTAGAGCCAGACTCTGAGAGG 768
Db ACAGACCTGGTTCCCTGCTCTGCAATTCAGGTGTGGTGGCTAGAGCCAGACTCTGAGAGG 1036
769 GTCCAAATTCCTGCTCCCTTTCCGGGAAGATCCCGGTGCAACAGGAACTCTGCGCACATAGCC 828
Db GTCCAAATTCCTGCTCCCTTTCCGGGAAGATCCCGGTGCAACAGGAACTCTGCGCACATAGCC 1096
829 AGGTGCGGTACTGTCTCCAGGGGTATGCGAGCTAGATGCGCTGTCTGTCTGCGCGGC 888
Db AGGTGCGGTACTGTCTCCAGGGGTATGCGAGCTAGATGCGCTGTCTGTCTGCGCGGC 1156
889 AAGGTAACTGTGCTGGCAGGACACAGACAGAGTCCCTGCCAGCCACTTGTGTGCCACCA 948
Db AAGGTAACTGTGCTGGCAGGACACAGACAGAGTCCCTGCCAGCCACTTGTGTGCCACCA 1216
949 GTGCCCCAGAAAGAACCACTGTGATGAGCCACAGATTTTCAGTTTGTGGCAGGCCAC 1008
Db GTGCCCCAGAAAGAACCACTGTGATGAGCCACAGATTTTCAGTTTGTGGCAGGCCAC 1276
1009 CCCAACCTCTGTGTCCAGGTGAGCACCTGGGAGAAGTTTCAGCTGCAAGCGTCTCGTGG 1068
Db CCCAACCTCTGTGTCCAGGTGAGCACCTGGGAGAAGTTTCAGCTGCAAGCGTCTCGTGG 1336
1069 GCTGACTCTGTGGGCCCTTCAAGGATGATATGCTGTGTAGTGAGATGAATAACCGGCTC 1128
Db GCTGACTCTGTGGGCCCTTCAAGGATGATATGCTGTGTAGTGAGATGAATAACCGGCTC 1396
1129 AACAAACATCATGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1188
Db AACAAACATCATGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1456
1189 TCCACGAGAGCTGCTCGCTGGGAGGAGTTTCTGCAAGACTTCCGATCACACCAAGTGT 1248
Db TCCACGAGAGCTGCTCGCTGGGAGGAGTTTCTGCAAGACTTCCGATCACACCAAGTGT 1516
1249 ATGACGTGTGGAACGATGACATGAGGATTCGCTATGGGCTTCGCCCATGGAAGATAC 1308
Db ATGACGTGTGGAACGATGACATGAGGATTCGCTATGGGCTTCGCCCATGGAAGATAC 1576
1309 ATCCACAGGCGTGGTCTCTAGTATGCTGCGCTGCTCTCTGCTGCGGCGCTTTTC 1368
Db ATCCACAGGCGTGGTCTCTAGTATGCTGCGCTGCTCTCTGCTGCGGCGCTTTTC 1636
1369 TTCTTCTCTCTTAAAAAGGACCGCAGGAAGCGCGCTGCTCCGACAGCGCTTG 1428
Db TTCTTCTCTCTTAAAAAGGACCGCAGGAAGCGCGCTGCTCCGACAGCGCTTG 1696
1429 CTCTTCACTCCCGCAGAGCGGCTACGAGCGTCTGTGGGAGCACTGGCGTCCGCG 1488
Db CTCTTCACTCCCGCAGAGCGGCTACGAGCGTCTGTGGGAGCACTGGCGTCCGCG 1756
1489 TTGAGCCAGATGCACTGCGCGTGGCGTGGACTGTGGAGCGCGCGAGCTGAGCGCG 1548
Db TTGAGCCAGATGCACTGCGCGTGGCGTGGACTGTGGAGCGCGCGAGCTGAGCGCG 1816
1549 CAGGAGCCCTAGCTGTGTTCCACCAACGAGCGCGCTATCTGAGGAGGTTGCGGTG 1608
Db CAGGAGCCCTAGCTGTGTTCCACCAACGAGCGCGCTATCTGAGGAGGTTGCGGTG 1876
1609 GTAATCTTCTTCTGCGCGCGCGGTGGCGCAGTGTGAGCAGTGGCTGCACTCCAG 1668
Db GTAATCTTCTTCTGCGCGCGCGGTGGCGCAGTGTGAGCAGTGGCTGCACTCCAG 1936
1669 ACAGTGGAGCCCGGGCGCATGACGCCCTCGCGCGCTGCTGCTGCTGCTACCGAT 1728
Db ACAGTGGAGCCCGGGCGCATGACGCCCTCGCGCGCTGCTGCTGCTGCTACCGAT 1996
1729 TTCTTCAAGCGCGCGCGACCGGCGCTACGTGCGGCTTACTTTCAGCGGCTGCTGCAC 1788
Db TTCTTCAAGCGCGCGCGACCGGCGCTACGTGCGGCTTACTTTCAGCGGCTGCTGCAC 2056

1789 CCAGACTCTGTGCTCCCTCCCGTTCCGCTGCGCGCGCTCTTCTCCCTGCCACGAGCTG 1848
Db CCAGACTCTGTGCTCCCTCCCGTTCCGCTGCGCGCGCTCTTCTCCCTGCCACGAGCTG 2116
1849 CCGGCTTTCTCGATGCACTGCAAGGAGGCTGCTCCACTTCCGCGGGGACCCCGGGAC 1908
Db CCGGCTTTCTCGATGCACTGCAAGGAGGCTGCTCCACTTCCGCGGGGACCCCGGGAC 2176
1909 CCGGTGGAAACGAGTGAACCCAGCGCTGCGGTCCGCTCGGACCTGGGACCTGCACTACAGAA 2022
Db CCGGTGGAAACGAGTGAACCCAGCGCTGCGGTCCGCTCGGACCTGGGACCTGCACTACAGAA 2236
1969 GAAGCCCCAGGCTGCTCGGAGGAATGGACCTGGGACCTGCACTACAGAA 2022
Db GAAGCCCCAGGCTGCTCGGAGGAATGGGACCTGGGACCTGCACTACAGAA 2290

RESULT 5
ABL34982
ID ABL34982 standard; cDNA; 2128 BP.
XX ABL34982;
AC
XX AC
DT 04-APR-2002 (first entry)
XX
DE Murine cDNA isolated from skin cells SEQ ID NO: 487.
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnery;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.
XX Mus sp.
OS
XX WO200190357-A1.
PN
XX 29-NOV-2001.
PD
XX 24-MAY-2001; 2001WO-NZ000099.
PF
XX 24-MAY-2000; 2000US-0206650P.
PR
XX 25-JUL-2000; 2000US-0221232P.
PR
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG;
PI Kumble KD;
PI
XX WPI; 2002-122020/16.
DR
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses.
PT
XX Claim 1; Page 295; 466pp; English.
PS
XX The present invention provides the protein and coding sequences of cDNAs
XX isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention
XX
SQ Sequence 2128 BP; 387 A; 674 C; 626 G; 441 T; 0 U; 0 Other;

Query Match 95.6%; Score 1933.6; DB 6; Length 2128;
Best Local Similarity 96.4%; Pred No. 0;
Matches 2018; Conservative 0; Mismatches 4; Indels 72; Gaps 1;

XX		26-MAR-2002	(first entry)
DT		Mouse DNAX cytokine receptor subunit 7 (DCRS7) cDNA.	
XX			
DE		Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;	
XX		gene therapy; protein therapy; immunological disorder.	
KW		Mus musculus.	
OS			
XX			
FH	Key	Location/Qualifiers	
FT	CDS	199..2295	
FT		/tag= a	
FT		/product= "Mouse DCRS7"	
XX			
FN	WO200190358-A2.		
XX			
PD	29-NOV-2001.		
XX			
PF	23-MAY-2001; 2001WO-US016767.		
XX			
PR	24-MAY-2000; 2000US-0206962P.		
XX			
PA	(SCHE) SCHERING CORP.		
XX			
PI	Gorman DM;		
XX			
DR	WPI; 2002-106198/14.		
DR	P-PSDB; AAU11354.		
XX			
PT	Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide		
PT	useful for detecting antibodies generated in response to presence of		
PT	increased protein levels or immunological disorders.		
XX			
PS	Disclosure; Page 17-20; 148pp; English.		
XX			
CC	The invention relates to primate and rodent DNAX cytokine receptor		
CC	subunit (DCRS) polypeptides and the polynucleotides encoding them. The		
CC	receptors, or their portions may be useful as phosphate labelling enzymes		
CC	to label general or specific substrates. The subunits may also be		
CC	functional immunogens to elicit recognising antibodies, or antigens		
CC	capable of binding antibodies. A combination, e.g., including a DCRS can		
CC	be used as an immunogen for the production of antisera or antibodies		
CC	capable of distinguishing between other cytokine receptor family members.		
CC	A purified DCRS can also be used as a reagent to detect antibodies		
CC	generated in response to the presence of elevated levels of expression,		
CC	or immunological disorders which lead to antibody production to the		
CC	endogenous receptor. This sequence represents cDNA encoding the mouse		
CC	DCRS7 polypeptide		
XX			
SQ	Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;		
	Query Match	95.6%; Score 1933.6; DB 6; Length 2314;	
	Best Local Similarity	96.4%; Pred. No. 0;	
	Matches 2018; Conservative	0; Mismatches 4; Indels 72; Gaps 1	
Qy	1 ATGCCTGTGTCCTGGTTCTGCTGCTTGGCACTGGGCCGAAACCTGTGGTGCTCT	60	
Dd	199 ATGCCTGTGTCCTGGTTCTGCTGCTTGGCACTGGGCCGAAACCTGTGGTGCTCT	258	
Qy	61 CTGGAGAGACTGATGAGCCTCAGAGACTGCACGCTGCTCTTAGGCCTCTCTCGCCAC	120	
Dd	259 CTGGAGAGACTGATGAGCCTCAGAGACTGCACGCTGCTCTTAGGCCTCTCTCGCCAC	318	
Qy	121 CTCTGGATGGTGAAGTGTCTGTGCTGGCTGGAGCCTCCAGTCTGCCCGCCCTGTG	180	
Dd	319 CTCTGGATGGTGAAGTGTCTGTGCTGGCTGGAGCCTCCAGTCTGCCCGCCCTGTG	378	
Qy	181 CTAGTGCCTACC CGCCTGCAGACGAGCTGTGTGCTGAGTGTCCACAGAAGACAGATTGC	240	
Dd	379 CTAGTGCCTACC CGCCTGCAGACGAGCTGTGTGCTGAGTGTCCACAGAAGACAGATTGC	438	
Qy	241 GCCCTCCGTGTCCTGGTGGTGCACCTGTCCTGGCCCGTGCATGGGCACCTGGGCAGAGCCTGAA	300	

1519 ATGAGCTGTGGAACGATGACACATGGGATCGCTATATGGGCTGCCCATGACAGTAC 1578
1309 ATCCACAGCGCTGGTCTAGTATGGCTGGCTGCTTACTTCTTGGCTGGCGCTTTTC 1368
1579 ATCCACAGCGCTGGTCTAGTATGGCTGGCTGCTTACTTCTTGGCTGGCGCTTTTC 1638
1369 TTCTTCTCTCTTCTTAAAGAGACCGCAGGAAAGCGGCCCGCTGCTCCCGCAGCGCTTG 1428
1639 TTCTTCTCTCTTCTTAAAGAGACCGCAGGAAAGCGGCCCGCTGCTCCCGCAGCGCTTG 1698
1429 TTCTTCTCTCTTCTTAAAGAGACCGCAGGAAAGCGGCCCGCTGCTCCCGCAGCGCTTG 1488
1699 TTCTTCTCTCTTCTTAAAGAGACCGCAGGAAAGCGGCCCGCTGCTCCCGCAGCGCTTG 1758
1489 TTGAGCGAGATGCCACTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1548
1759 TTGAGCGAGATGCCACTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1818
1549 CACGAGCGCTTACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1608
1819 CACGAGCGCTTACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1878
1609 GTAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1668
1879 GTAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1938
1669 ACAGTGGAGCG 1728
1939 ACAGTGGAGCG 1998
1729 TTCTTCTGCAAGCG 1788
1999 TTCTTCTGCAAGCG 2058
1789 CAGAGCTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1848
2059 CAGAGCTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2118
1849 CCGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1908
2119 CCGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2178
1909 CCGGTGGAACAGATGACCCAGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1968
2179 CCGGTGGAACAGATGACCCAGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2238
1969 GAAGCCCGAGGCTCTCGGAGGATGGAGCTGGAGCCCTGCACTACACTAGAA 2022
2239 GAAGCCCGAGGCTCTCGGAGGATGGAGCTGGAGCCCTGCACTACACTAGAA 2292

RESULT 7
AEB55651 ID AEB55651 standard; cDNA; 2314 BP.
XX AC AEB55651;
XX AC AEB55651;
DT 22-SEP-2005 (first entry)
DE Mouse DCSR7 polypeptide encoding cDNA.
XX Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
XX DCSR; interleukin-17c; IL-17c; psoriasis; inflammatory bowel disorder;
XX interstitial lung disorder; asthma; allergy; atherosclerosis;
XX gastrointestinal-gen.; antiinflammatory; antiaesthetic; antiallergic;
XX antipsoriatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
XX antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17c antagonist;
XX IL-17c agonist; mouse; DCSR7; gene; ss; antisense therapy; RNAi therapy.
XX Mus musculus.
XX OS
XX Key Location/Qualifiers
XX FH 199. .2295
XX CDS

FT FT /*tag= c /product= "DCRS7"
FT mat_peptide /199. .2292
FT /*tag= b
FT sig_peptide /199. .258
FT /*tag= a
XX W02005065711-A2.
PN 21-JUL-2005.
XX 22-DEC-2004; 2004WO-US042935.
XX 29-DEC-2003; 2003US-00749144.
XX (SCHE) SCHERING CORP.
XX Gorman DM;
XX WPI; 2005-506792/51.
XX P-PSDB; AEB55652.
DR Modulating activity of cell, involves contacting cell with an agonist or
XX antagonist of DNAX cytokine receptor subunit.
XX Example 5; SEQ ID NO 7; 130pp; English.
XX The invention relates to modulating (M1) activity of cell, by contacting
XX cell with an agonist or antagonist of DNAX cytokine receptor subunit
XX (DCRS9) or of interleukin (IL-17c where the cell modulates psoriasis,
XX inflammatory bowel disorder (IBD), interstitial lung disorder, asthma, or
XX allergy, or atherosclerosis. Also provided are methods for treating (M2)
XX the disorders which involves administration of the modulator and
XX diagnosing (M3) a disorder as mentioned above that involves contacting a
XX sample from a test subject with a binding composition that specifically
XX binds to a polypeptide or nucleic acid of DCSR9 or IL-17c. (M1) is useful
XX for modulating an activity of a cell. (M2) is useful for treating a
XX subject suffering from a disorder such as psoriasis, IBD, interstitial
XX lung disorder, asthma or allergy, or atherosclerosis, where the
XX interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
XX granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
XX ulcerative colitis. The present sequence represents a mouse DCSR7
XX polypeptide encoding cDNA.
XX Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;

Query Match 95.6%; Score 1933.6; DB 14; Length 2314;
Best Local Similarity 96.4%; Pred No. 0;
Matches 2018; Conservative 0; Mismatches 4; Indels 72; Gaps 1;
QY 1 ATGCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 199 ATGCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
QY 61 CTGGAGAGACTGATGGAGCCTCAGGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 259 CTGGAGAGACTGATGGAGCCTCAGGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
QY 121 CTCTGGATGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 319 CTCTGGATGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
QY 181 CTAGTGCCTACCCGCTGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 379 CTAGTGCCTACCCGCTGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
QY 241 GCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 439 GCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
QY 301 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTAGGACGCTCTCTCCAGGCCCGAG 360
Db 499 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTAGGACGCTCTCTCCAGGCCCGAG 558

Qy	361	GTG	TGCTCTCTTTCAGG	CCCTACCCCATCGCCCGCTGTG	CCCTGCTGGAAGTCCAG	GTG	420
Db	559	GTG	TGCTCTCTTTCAGG	CCCTACCCCATCGCCCGCTGTG	CCCTGCTGGAAGTCCAG	GTG	618
Qy	421	CCC	GCTGACCTGTGTG	CGCCGTGTGCTCAGT	CGGTGGTTCGGGTATTTG	ACTGTTTCG	480
Db	619	CCC	GCTGACCTGTGTG	CGCCGTGTGCTCAGT	CGGTGGTTCGGGTATTTG	ACTGTTTCG	678
Qy	481	GCT	AGTCTTTGGGGCTG	AGGTACAGATCTGTGCTTAC	ACGAAGCCAGGTAC	CAGAAAGAG	540
Db	679	GCT	AGTCTTTGGGGCTG	AGGTACAGATCTGTGCTTAC	ACGAAGCCAGGTAC	CAGAAAGAG	738
Qy	541	CTC	AACCTTCACACAG	CGCTGCTT-----	-----	-----	564
Db	739	CTC	AACCTTCACACAG	CGCTGCTT-----	-----	-----	798
Qy	565	-----	-----	-----	-----	-----	588
Db	799	AGT	GTGCGGTCTG	CGCCCTGCTCAATGTGTCTA	CAGATGCTGTA	CAATGCTTCTG	858
Qy	589	CTG	ATGTCTCTGAGG	AGCAGACTTTTAGCTTCTT	ACTGTACCTCGCTC	CAGATCCCGGAT	648
Db	859	CTG	ATGTCTCTGAGG	AGCAGACTTTTAGCTTCTT	ACTGTACCTCGCTC	CAGATCCCGGAT	918
Qy	649	GCT	CTCAAACTCTTGT	TGGTCAAAAACTCTA	CTGGACCTCAGAACTAT	CTTTAAACCA	708
Db	919	GCT	CTCAAACTCTTGT	TGGTCAAAAACTCTA	CTGGACCTCAGAACTAT	CTTTAAACCA	978
Qy	709	AC	AGACCTGGTTCCT	CGCTCTGCAATCAAGTGTGTG	CTAGAGCCAGACTCTG	AGAGG	768
Db	979	AC	AGACCTGGTTCCT	CGCTCTGCAATCAGTGTGTG	CTAGAGCCAGACTCTG	AGAGG	1038
Qy	769	GT	CGAATTCGCCCCT	TCGCGGAGATCCCGGTG	CCACAGGAACCTCTG	CGCATAGCC	828
Db	1039	GT	CGAATTCGCCCCT	TCGCGGAGATCCCGGTG	CCACAGGAACCTCTG	CGCATAGCC	1098
Qy	829	AG	GCTGCGGGTACT	GTGCTCCACAGGGGTATG	GCACTAGATCGCCTT	GCTGTCTGCGCGGC	888
Db	1099	AG	GCTGCGGGTACT	GTGCTCCACAGGGGTATG	GCACTAGATCGCCTT	GCTGTCTGCGCGGC	1158
Qy	889	AAG	GTAACTGTGTCTG	GGCAGGCCACAGAC	CCAGAGTCCCTG	CGCAGCCACCA	948
Db	1159	AAG	GTAACTGTGTCTG	GGCAGGCCACAGAC	CCAGAGTCCCTG	CGCAGCCACCA	1218
Qy	949	GT	CCCCCAGAGAAC	CGCCTGTGAATGAGCC	CAAGATTTCCAGTTTGGT	TGGCAGGGCCAC	1008
Db	1219	GT	CCCCCAGAGAAC	CGCCTGTGAATGAGCC	CAAGATTTCCAGTTTGGT	TGGCAGGGCCAC	1278
Qy	1009	CCC	AACCTCTGTGTCT	GAGTGTAGCACCTGG	GAGAGGTTCAGCTG	CAAGCGTGTCTGTG	1068
Db	1279	CCC	AACCTCTGTGTCT	GAGTGTAGCACCTGG	GAGAGGTTCAGCTG	CAAGCGTGTCTGTG	1338
Qy	1069	GCT	GACTCTCTTGGG	CCCTTCAAGGATGATATG	CTGTAGTGGAGATG	AAAAACGGGCTC	1128
Db	1339	GCT	GACTCTCTTGGG	CCCTTCAAGGATGATATG	CTGTGTAGTGGAGATG	AAAAACGGGCTC	1398
Qy	1129	AAC	AAACATCAGTCTG	TCCTTGGAAACCCAGTGG	CTGTGTACCACTG	CCCCAGGATGGCC	1188
Db	1399	AAC	AAACATCAGTCTG	TCCTTGGAAACCCAGTGG	CTGTGTACCACTG	CCCCAGGATGGCC	1458
Qy	1189	TCC	ACGAGAGTCTG	CTCGCTCGGGAGAGG	TGCTGCAAGACTTCC	GATCACCAGTGT	1248
Db	1459	TCC	ACGAGAGTCTG	CTCGCTCGGGAGAGG	TGCTGCAAGACTTCC	GATCACCAGTGT	1518
Qy	1249	AT	GAGCTGTGGA	ACGATGACCAATGGGAT	CTGCTATGGGCT	CGCCCATGGACAGTAC	1308
Db	1519	AT	GAGCTGTGGA	ACGATGACCAATGGGAT	CTGCTATGGGCT	CGCCCATGGACAGTAC	1578
Qy	1309	AT	CAAGGCGCTGG	GTCTTAGTATGCTGG	CTGCTACTCTTGG	CTGGGCGCTTTTC	1368
Db	1579	AT	CAAGGCGCTGG	GTCTTAGTATGCTGG	CTGCTACTCTTGG	CTGGGCGCTTTTC	1638

QY	1369	TTCTTCTCTCTTTCTTAA	AAAGACCGCAGAGAAAGCGCGTGGCTCCCGCAGCGGCTTG	1428
Db	1639	TTCTTCTCTCTTTCTTAA	AAAGACCGCAGAGAAAGCGCGTGGCTCCCGCAGCGGCTTG	1698
QY	1429	CTCTCCACATCCGCGCAG	CGGAGCGGCTACGAGGCTTGTGTGGAGACATGGCGTCCGCG	1488
Db	1699	CTCTCCACATCCGCGCAG	CGGAGCGGCTACGAGGCTTGTGTGGAGACATGGCGTCCGCG	1758
QY	1489	TTGAGCCAGATGCCACTC	GTGCGCGTGGCCGTGGACCTGTGTGGAGCCGCCCGCAGAGCTGAGCGCG	1548
Db	1759	TTGAGCCAGATGCCACTC	GTGCGCGTGGCCGTGGACCTGTGTGGAGCCGCCCGCAGAGCTGAGCGCG	1818
QY	1549	CACGGAGCCCTAGCCTGT	TCCACACACCGACCGCGCTATCTGTGACGAGGCTGCGCGT	1608
Db	1819	CACGGAGCCCTAGCCTGT	TCCACACACCGACCGCGCTATCTGTGACGAGGCTGCGCGT	1878
QY	1609	GTAATCTTCTTCTCTCT	CGCCGCGCGTGGCGAGTGTTCAGCATGGCTGTGACAGTCCAG	1668
Db	1879	GTAATCTTCTTCTCTCT	CGCCGCGCGTGGCGAGTGTTCAGCATGGCTGTGACAGTCCAG	1938
QY	1669	ACAGTGAGCCCGGGCGC	ATGACGCCCTCGCCGCTGGCTCAGCTGCGTGTACCCGAT	1728
Db	1939	ACAGTGAGCCCGGGCGC	ATGACGCCCTCGCCGCTGGCTCAGCTGCGTGTACCCGAT	1998
QY	1729	TTCTCTCAAGCCGGGCG	CACCGCGCTACGTCGGGCTCTATTTCGACGGGCTGTGCGAC	1788
Db	1999	TTCTCTCAAGCCGGGCG	CACCGCGCTACGTCGGGCTCTATTTCGACGGGCTGTGCGAC	2058
QY	1789	CCAGACTCTGTGCGCTC	CGCGTTCGGCGTCCCGCTCTTCTCTGCCCCAGCGAGCTG	1848
Db	2059	CCAGACTCTGTGCGCTC	CGCGTTCGGCGTCCCGCTCTTCTCTGCCCCAGCGAGCTG	2118
QY	1849	CCGCGCTTCTTGATGAC	TGACGAGGAGGCTGCTCCACTTCCGCGGGGCGACCCCGGAC	1908
Db	2119	CCGCGCTTCTTGATGAC	TGACGAGGAGGCTGCTCCACTTCCGCGGGGCGACCCCGGAC	2178
QY	1909	CGGCTGAACGAGTGAC	CCAGCGCGCTCGGTCGCCCTTGGACAGCTGTACTTCTAGCTCG	1968
Db	2179	CGGCTGAACGAGTGAC	CCAGCGCGCTCGGTCGCCCTTGGACAGCTGTACTTCTAGCTCG	2238
QY	1969	GAAGCCCCAGGCTGCTG	CGAGGAAATGGGACCTGGGACCTGCACTACATAGAA	2022
Db	2239	GAAGCCCCAGGCTGCTG	CGAGGAAATGGGACCTGGGACCTGCACTACATAGAA	2292
RESULT 8				
ABK86568				
ID	ABK86568 standard; cDNA; 2331 BP.			
XX				
AC	ABK86568;			
XX				
DT	24-SEP-2002 (first entry)			
XX				
DE	Mouse interleukin 17 receptor like protein, IL-17RL, full length cDNA.			
XX				
KW	Mouse; ss; gene; Interleukin 17 receptor-like protein; IL-17RL;			
KW	chondrolectin; bone degradation; cartilage degradation; gene therapy;			
KW	chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;			
KW	allergic skin immune response; organ transplant rejection; cyclokinine;			
KW	osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;			
XX	seronegative spondyloarthropathy; bone morphogenetic protein.			
OS	Mus sp.			
XX				
Key	Location/Qualifiers			
FT	199..2295			
CDS	/*tag= a			
FT	/*product= "IL-17RL"			
FT	/*transl_except= (pos:2077..2079,aa:Xaa)			
FT	/*transl_except= (pos:2161..2163,aa:Xaa)			
FT	/*transl_except= (pos:2200..2202,aa:Xaa)			
FT	/*transl_except= (pos:2242..2244,aa:Xaa)			
FT	/*note= "Xaa is unknown"			

[illegible]

	1549	TCCACGAGAGCTGCTCGCTGGGAGAGGAGTGTCTGCAGACTTCGATCACCAGTGTT	1511
D _b			
Q _y	1249	ATGCAGCTGTGGAAACGATGACAACATGGGATCGCTATGGGCCCTGCCCATGGCAACAGTAC	1308
D _b			
	1519	ATGCAGCTGTGGAAACGATGACAACATGGGATCGCTATGGGCCCTGCCCATGGCAACAGTAC	1578
Q _y	1309	ATCCACAGGCGCTGGGTTCTTAGTATAGCTTGGCTGGCCCTGCTACTCTTTGGCTTGGCGCGCTTTTC	1368
D _b			
	1579	ATCCACAGGCGCTGGGTTCTTAGTATAGCTTGGCTGGCCCTGCTACTCTTTGGCTTGGCGCGCTTTTC	1638
Q _y	1369	TTCTTCTCTCTTCTTAATAAAGAGCACGCGAAGAAGCGGCCGTGGCTCCC CGCACGGCCCTTG	1428
D _b			
	1639	TTCTTCTCTCTTAAATAAAGAACCGCAGGAAGCGGCCGTGGCTCCC CGCACGGCCCTTG	1698
Q _y	1429	CTCTCCACTCCGCCGACGAGCGGGCTACGAGCGTCTGTGTGGAGACACTGGCGTCCGCG	1488
D _b			
	1699	CTCTCCACTCCGCCGACGAGCGGGCTACGAGCGTCTGTGTGGAGACACTGGCGTCCGCG	1758
Q _y	1489	TTGAGCCAGATGCCACTTGGCGGTGGCGTGGACCTGTGGAGCGCCCGCGAGCTGTAGGCGG	1548
D _b			
	1759	TTGAGCCAGATGCCACTTGGCGGTGGCGTGGACCTGTGGAGCGCCCGCGAGCTGTAGGCGG	1818
Q _y	1549	CACGGAGCCCTAGCTCGTGTCCACCAACAGCGACCGCGTATCTCTGCAGGAGGGTGGCGTG	1608
D _b			
	1819	CACGGAGCCCTAGCTCGTGTCCACCAACAGCGACCGCGTATCTCTGCAGGAGGGTGGCGTG	1878
Q _y	1609	GTAATCTCTCTTCTCGCCCGCGCGCTGGCGCAGTGTGACGAGTGGCTGCAGCTCCAG	1668
D _b			
	1879	GTAATCTCTCTTCTCGCCCGCGCGCTGGCGCAGTGTGACGAGTGGCTGCAGCTCCAG	1938
Q _y	1669	ACAGTGGAGCCCCGGGCCGCAATGACGCCCTCGCCGCCCTGGCTCAGCTGCTGCTACCCGAT	1728
D _b			
	1939	ACAGTGGAGCCCCGGGCCGCAATGACGCCCTCGCCGCCCTGGCTCAGCTGCTGCTACCCGAT	1998
Q _y	1729	TTCTTGCAGGCGCGGGCGACCGCGCGCTACGTGGGGTCTACTTCGACGGGCTGCTGCAC	1788
D _b			
	1999	TTCTTGCAGGCGCGGGCGACCGCGCGCTACGTGGGGTCTACTTCGACGGGCTGCTGCAC	2058
Q _y	1789	CCAGACTCTGTGCCTCTCCCGCTTCGCGGTGGCCCGCTCTTCTCCCTGCCACGCGCAGCTG	1848
D _b			
	2059	CCAGACTCTGTGCCTCTCCGS TTCCGGGTTCGCGGTTCGCGGTCTCTTCTCCCTGCCAGCTG	2118
Q _y	1849	CCGGCTTTCCTGGATGCACTGCAGGGAGGCTGCTCCA TTTCCGCGGGCGACCCCGGGAC	1908
D _b			
	2119	CCGGCTTTCCTGGATGCACTGCAGGGAGGCTGCTCCA TTTCCGCGGGCGACCCCGGGAC	2178
Q _y	1909	CGGGTGGACGAGTGACCCAGGCGCTGGGCTCGCCCTCGACAGACTGTACTTCTAGCTCG	1968
D _b			
	2179	CGGGTGGACGAGTGACCCAGGCGCTGGGCTCGCCCTCGACAGACTGTACTTCTAGCTCG	2238
Q _y	1969	GAAGCCCCAGGCTGCTCGAGGAAATGGACCTGGGACCTTCGCACTACACTAGAA	2022
D _b			
	2239	GAASCCCCAGGCTGCTCGAGGAAATGGACCTGGGACCTTCGCACTACACTAGAA	2292
RESULT 9			
AAD24221			
ID	AAD24221	standard; DNA; 2022 BP.	
XX	AC	AAD24221;	
XX	AC		
XX	DT	17-MAY-2002 (first entry)	
XX	XX	Murine cytokine receptor, Zcytorl4 degenerate DNA.	
DE	XX		
XX	XX	Murine; cytokine receptor; Zcytorl4; inflammation; rheumatoid arthritis;	
KW	XX	gene therapy; protein therapy; ds.	
XX	OS	Mus sp.	
XX	OS		
PN	XX	WO200204519-A2.	
XX	PD	17-JAN-2002.	

[illegible]

QY	481	GCTAGCTTGGGCTGAGTACAGATCTGCTCTACACAGAGCCAGGTACACAGAAAGAG	540	1561	GCTGTGTTCCACACACAGCAGCGGTATCTCTGAGGAGGGTGGCGTGAATCTTCTC	1620
Db	481	GCNWSNYTNGNGCNGARGTNCARATHGHSNTAYACNAARCCNMGNATYCARAARGAR	540	1561	GCNTGTGTTTCAYCAYCARMGNMGNATHYTNCAARGAGGNGTNGTNTATHYTNYN	1620
QY	541	CTCAACCTCACACAGACCTCCCTGATGGTGAACATGCTCTTCTGACACTGGATGCTCT	600	1621	TTCTCCGCCCGCGCGGTGGCGAGTGTGACAGTGTGCTGAGTGGCTGACAGACTGGAGCC	1680
Db	541	YTNAAYYTNACNARCARYTNCNGAYGGNGAYAAAGTNYTNYTACNYTNGAYGTWNS	600	1621	TTWNSCCNGCNGCNGTNGCNCARTGYCARCARTGGYTNCARTYTNCAACNGTNGARCN	1680
QY	601	GAGGAGCAGGACTTAGCTTCTTACTGTACTGTGCTCCAGTCCCGGATGCTCTCAAAATCC	660	1681	GGGCCCATGAGCCCTCGCGCTGAGTGTGCTGCTGCTGCTACCCGATTTCTCTGCAAGGC	1740
Db	601	GARGARCARGATYTTWNSNTYNTAYTNYTNGCNGCNGTNGCNGAYGCMYTNAAWSN	660	1681	GNCCNCAVAYGCTNYTNGCNGTNGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
QY	661	TTGTGCTCAAAACCTCACTGGAACCTCAGAACATTAATCTTAAACCAACACAGACTGCT	720	1741	CGGGCAGCCGCGCTACGTCGCGGTCTACTTCCGAGCGGCTGCTGCTGCTGCTGCTG	1800
Db	661	YNTGCTAYARAYTNYTNGCNGCNCARAAATACNATYTNAAVCAVACNGAYTNGTN	720	1741	MGNCCNACNGMNTAYTNGGNGTNTAYTGYGNYTNTYCNAYCNGAYWNSNGTN	1800
QY	721	CCCTGCTCTCATTCAGTGTGCTGCTGAGCAGACTCTGAGAGGCTCGAATCTGCTG	780	1801	CCCTCCCGCTTCCGCTCGCGCTCTTCTCCCTGCCACGAGCTGCGGGCTTTCCTG	1860
Db	721	CCNTGYTNTGYATHCARGTNTGWSNTYTNAGCNGAYWNSGARMGNTGARTTYGY	780	1801	CCNWSNCNTTNGNGTNGCNCNTTNTTWSNYTNCNACNARYTNCNGCNTTYTN	1860
QY	781	CCCTTCCGGAAGATCCCGTGCACACAGAACCTCTGCGACATAGCCAGGCTCGGGTA	840	1861	GATGCACTGCAGGAGGCTGCTCCTCACTTCGCGGGGCGACCCCGGACCGGGTGGACGA	1920
Db	781	CCNTTYMGARGAYCCNGGNGCNCAYMGNAAYYTNTGGCAVATHGCMNYTNGCNGTN	840	1861	GAYGCTTNCARGNGGNTGYWNAWNNGCNGMNCNGCNGAYMGNGTNGARMGN	1920
QY	841	CTGTCCCGAGGGTATGGCAGCTAGATGCGCTTGTCTGCTCGCGGCAAGTAACTG	900	1921	GTGACCCAGCGCTGCGGCTCGCGCTGAGCAGCTGCTACTTCTAGCTCGGAAGCCGAGGC	1980
Db	841	YTNWSNCNGGNTTNGCARYTNGAYGNCNTGYTGYTNCNGNAAAGTNAACNTYN	900	1921	GTNACNARGCNTNMGNWSNGTNGAYWNSNTGYACNWSNWSNNGARGCNCNGN	1980
QY	901	TGCTGGAGGCCACACAGACTGCTCGCAGCCTTGTGCGCAGCTGCGCCAGAG	960	1981	TGCTGCGAGGAGTGGGACCTGGGACCTGCACTACACTAGAA	2022
Db	901	TGYTGGCARGCNCNGAYCARNSNCNTGYCARCNYTNGTNCNGCNGTNCNCABAR	960	1981	TGYTGYGARGARTGGGAYTNGGNCNTGYACNACNYTNGAR	2022
QY	961	AACGCCACTGTGAATGAGCCACAGATTTCCAGTTGGTGGCGAGCCACCCCACTCTGT	1020	RESULT 10		
Db	961	AATGCMNCNTNAYGARCCNARGATYTCARYTNGTNGCNGCNGCAYCCNAAVYNTGY	1020	AAD24223	standard; DNA; 2094 BP.	
QY	1021	GTCCAGTGTGACCTGGGAGAGGTTACGCTCAAGCGTGTCTGCGGCTGACTCTCTG	1080	ID	AAD24223	
Db	1021	GTNCARGTNWSNACNTGGGARAARGTNCARYTNCARGCNTGYWNSNTGGGCGGAYSNYN	1080	XX		
QY	1081	GGGCCCTCAAGATGATGCTGTAGTGAGATGAAACCGGCTCAACACACATCA	1140	AC	AAD24223;	
Db	1081	GGNCNTTYAARGAYATGYTNYTNGTNGATGAARACNGYTNAAVAYACNWSN	1140	DT	17-MAY-2002 (first entry)	
QY	1141	GTCTGTGCTTGGAACCCAGTGGCTGACCACTGCGCCAGCATGCGCTCCAGAGCT	1200	DE	Murine Zcytor14 cytokine receptor variant, Zcytor14-1 degenerate DNA.	
Db	1141	GTNTGYGCTNGARCCNWSNGNTGYACNCCNTNCNWSNATGCGCNCNMGNGN	1200	XX	Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;	
QY	1201	GCTCGCTGGGAGAGGATGCTGCAAGACTTCCGATCACACAGTGTATGAGCTGTGG	1260	XX	gene therapy; protein therapy; Zcytor14-1; ds.	
Db	1201	GCNNGTNGGARGARYTNYTNCARGAYTNYTNGWNSCAYCARTGYATGARYTNG	1260	OS	Mus sp.	
QY	1261	AACGATGACAACTGGATGCTATGGGCTGCGCCATGGAACAAGTACATCCAGCGC	1320	XX	WO200204519-A2.	
Db	1261	AAVAYGAYATGGGWSNYTNGGCTGCGATGAYAAATAYATHCAVGMNGN	1320	XX	17-JAN-2002.	
QY	1321	TGGGTCTTAGTGTGCTGCTGCTACTCTGCTGCGGCTTCTCTCTCTCTCT	1380	XX	05-JUL-2001; 2001WO-US021344.	
Db	1321	TGGGTNTGNTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380	XX	06-JUL-2000; 2000US-0216446P.	
QY	1381	CTAAAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1440	XX	(ZYMO) ZYMOGENETICS INC.	
Db	1381	YTNAAARGAYMGNMGAARCCNGCNGCNGGNGNWSNMGNAACNGCNYTNYTNCAYWSN	1440	XX	Gao Z;	
QY	1441	GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1500	XX	WPI; 2002-179701/23.	
Db	1441	GCNAYGNGCNGGNTAYGARMGNTNGTNGCNGCNGTNGCNGCNGTNYTWSNARATG	1500	XX	New murine cytokine receptor, Zcytor14, and polynucleotides encoding the	
QY	1501	CCACTGCGGCTGGGCTGAGCTGAGCAGCGCGGAGCTGAGCGCGCAGGAGCCCTA	1560	PT	receptor, useful for treating inflammation, specifically rheumatoid	
Db	1501	CCNYTNGMGTNGCTGATYNTTGGWSNMGNMGNARGARYTWSNCGNCAYGGGNCNTN	1560	PT	arthritis, and as educational tools or in research.	
				XX	Claim 8; Page 97-98; 99pp; English.	
				XX	The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14	
				XX	polypeptide is useful for identifying or isolating Zcytor14 ligands, in	
				XX	preparing antibodies, in identifying proteins or peptide cleavage sites,	
				XX	in amino acid sequence analysis, and in monitoring biological activities	
				XX	of both the native and tagged protein in vitro or in vivo. Polypeptides	

[illegible]

1861	CCNGAYWSNGTNCNWSNCCNTTYMGNGTNGCNCNTYNTTYWSNTTNCNACNCARYTN	1920
1849	CCGGCTTTCTCGTGCATCTGCAGGAGGCTGCTCCACATTTCCCGGGGGCGACCCGGGAC	1908
1921	CNCGCMTTYTNGAYGCTYNTCARGGNGNTGYWSNACNWSNCGNGMNCNGCNGAY	1980
1909	CGGGTGGAAAGAGTGCACCCAGGCGCTGCGGCTCGCCCTGGACAGCTGTACTTCTAGCTCG	1968
1981	MENGTNGARWNGTNAACNARGCNYTNMGWSNCGNYTNGAYWSNTGYACNWSNWSN	2040
1969	GAAGCCCGGCTGCTGCGAGGAATGGACCTGGGACCTGCACTACACTAGAA	2022
2041	GARGCNCNGENTGYTGYGARGARTGGAYTNGCCTGYACNACNYTNGAR	2094

RESULT 11

AAS18133

ID

AAS18133 standard; cDNA; 2094 BP.

XX

AAS18133;

XX

26-MAR-2002 (first entry)

XX

Mouse DCRS7 reverse translation generic cDNA.

XX

Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;

XX

gene therapy; protein therapy; immunological disorder.

XX

Mus musculus.

XX

WO200190358-A2.

XX

29-NOV-2001.

XX

23-MAY-2001; 2001WO-US016767.

XX

24-MAY-2000; 2000US-0206862P.

XX

(SCHE) SCHERING CORP.

XX

Gorman DM;

XX

WPI; 2002-106198/14.

XX

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide

XX

useful for detecting antibodies generated in response to presence of

XX

increased protein levels or immunological disorders.

XX

Disclosure; Page 20-21; 148pp; English.

XX

The invention relates to primate and rodent DNAX cytokine receptor

XX

subunit (DCRS) polypeptides and the polynucleotides encoding them. The

XX

receptors, or their portions may be useful as phosphate labelling enzymes

XX

to label general or specific substrates. The subunits may also be

XX

functional immunogens to elicit recognising antibodies, or antigens

XX

capable of binding antibodies. A combination, e.g., including a DCRS can

XX

be used as an immunogen for the production of antisera or antibodies

XX

capable of distinguishing between other cytokine receptor family members.

XX

A purified DCRS can also be used as a reagent to detect antibodies

XX

generated in response to the presence of elevated levels of expression,

XX

or immunological disorders which lead to antibody production to the

XX

endogenous receptor. This sequence represents mouse DCRS7 reverse

XX

translation generic cDNA

XX

Sequence 2094 BP; 247 A; 251 C; 393 G; 285 T; 0 U; 918 Other;

XX

Query Match 65.7%; Score 1327.6; DB 6; Length 2094;

XX

Best Local Similarity 54.2%; Pred. No. 7.4e-283;

XX

Matches 1135; Conservative 465; Mismatches 422; Indels 72; Gaps 1

QY

1 ATGCGCTGCTCGTGGTTCTCTGCTGTCTCTGGCACTGGCGCGAAACCTGTGTCGTCTCT

60

Db	1531	TGCCTACTCTTTGCGCTGGCTTCCCTCATCTCTCTCAAAAAGGATCATCGCGAAA	1590
Qy	1402	GGGGCCCGTGGTCCCGCAGCGGCTTGTCTCTCACTCGCGCAGGAGCGGGTACGAG	1461
Db	1591	GGGGCCCGCAGGCGCGCGCGCTCTGTCTCTTACTCAGCGATGACTCGGGTTCCGAG	1650
Qy	1462	CGTCTGGTGGAGCACTGSCGTCGCGTTGAGCCAGATGCCACTCGCGTGGCCGCTGGAC	1521
Db	1651	CGCCTGGTGGGCGCCCTGCGCTGCGCTGTCAGCTGCGCTGCGCTGCGCTGCGCTAGAC	1710
Qy	1522	CTGTGAGAGCGCGCGAGCTGAGCGCGCAGCGAGCCCTAGCCTGCTTCCACCAACAGCGA	1581
Db	1711	CTGTGAGCGCTGCTGAACCTGAGCGCAGGCGCGCTGGCTTTCACGCGCAGCGG	1770
Qy	1582	CGCGCTATCTGAGAGAGGCTGGCGTGAATCTTCTCTCGCCCGCGCGCTGGCG	1641
Db	1771	CGCCAGACCTGTCAGAGGCGCGCTGGTGGTCTTGTCTCTTCTCTCCCGCTGGCTGGCG	1830
Qy	1642	CAGTGTCAAGTGGCTGCA-----GCTCCAGACAGTGGAGCCCGGCGCGATGAC	1692
Db	1831	CTGTGAGCGAGTGGCTACAGGATGGGTGTCCGGCGCGCGCGCAGCGCGCGCAGAC	1890
Qy	1693	GCCCTCGCCCGCTGGCTCAGCTGCGTACCGGATTTCTGCAAGCGCGCGCGCGCGC	1752
Db	1891	GCCCTCGCGCTCGCTCAGCTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1950
Qy	1753	CGCTTACGCGGGTCTACTTTCGAGCGGCTGCTGCAACCGCGAGCTCTGTGCGCTCCCGTTC	1812
Db	1951	AGCTACGTTGGGGCGCTCTTTCGACAGGCTGCTCCACCGCGAGCGCTACCGCGCTTTC	2010
Qy	1813	CGCGTCCCGCGCTTCTCTCGCCCGCAGAGTGGCGCTTCTCTGAGTGCATGCTGAG	1872
Db	2011	CGCACCGTGGCGCTTCTCAGCTGCGCTCCCACTGCGCTTCTCTGCGCGCGCTTTC	2070
Qy	1873	GGAGGCTGCTCACTTCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1932
Db	2071	CAGCTTCGCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCGCGCGCG	2130
Qy	1933	CTGCGCTCGCGCGCGCGCTGAGCT-GTACTTCTGAGTTCGAGAGCGCGCGCGCGCGCG	1991
Db	2131	CTTACGCGCGCGCGCTGAGTACTTCTTCCATCCCGCGCGCGCGCGCGCGCGCGCGCG	2190
Qy	1992	ATGGAGCTGGGAC 2005	
Db	2191	GTGGACCGCGCGCG 2204	
RESULT 13			
AAD47894			
ID	AAD47894 standard; cDNA; 2255 BP.		
XX	AAD47894;		
AC	AAD47894;		
DT	12-FEB-2004 (first entry)		
XX	Human cytokine receptor Zcytor14 cDNA.		
DE	Cytokine receptor; Zcytor14; chromosome 3p25-3p24; cardiomyopathy;		
XX	xeroderma pigmentosum; Marfan-like connective tissue disorder;		
KW	diabetes mellitus; Fanconi anaemia; renal cell carcinoma; gene;		
KW	Marfan syndrome; Von Hippel-Lindau syndrome; blepharophimosis; human; ss.		
XX	Homo sapiens.		
XX	Key		
FX	Location/Qualifiers		
FT	154..2232		
FT	/*tag= a		
FT	/product= "Zcytor14 precursor protein"		
FT	154..213		
FT	/*tag= b		
FT	214..2229		
FT	/*tag= c		
FT	/product= "Mature Zcytor14 protein"		

Db	454	GATGAGGAAAAGTTTGGAGGAGAGCTGACTCAGGGGTGAGGAGCCTAGGATGCTCT	513
Qy	349	CTCAGAGCCAGGTGGTCTCTCTTCCAGGCTTACCCCATTCGCGCGCTGTGCGCTGCTG	408
Db	514	CTCAGGCGCAAGTCTGCTCTCTTCCAGGCTTACCCCATTCGCGCGCTGTGCGCTGCTG	573
Qy	409	GAGTCCAGGTGCGCGCTGACCTGTGTGAGCGCTGGTCACTGCGGTGCTGCGGTATTT	468
Db	574	GAGGTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	633
Qy	469	GACTGTTCAGGCTGAGTCTTGGGCTCAGGTACAGATCTGCTTCTACAGAACCCAGG	528
Db	634	GACTGCTTCAGGCTGCGCTTGGGCTCAGGTACAGATCTGCTTCTACAGAACCCAGG	693
Qy	529	TACCAAGAAAGCTCAACCTTCAACAGAGCTGCT-----	564
Db	694	TACGAGAGAACTCAACCAACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	753
Qy	565	---GATGTGACATGTCTCTTCTGACACTGGATGCTCTGAGGAGCAGGACTTTAGCTTC	621
Db	754	GCAGATGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	813
Qy	622	TACTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	681
Db	814	TCCCTGTACTGAGTCAAGTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	873
Qy	682	GGACCTCAGAAATTAATTAAACCAACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	741
Db	874	GGACCGCAGATCAATTAATTAAACCAACAGAGCTGCTGCTGCTGCTGCTGCTGCTG	933
Qy	742	TGCTGCTGAGAGCTGAGAGGCTGCAATCTGCGCGCTTCCGCGGAGATCCCGGT	801
Db	934	TGGCTCTGGAACCTGACTCCGTTAGACGCAATCTGCGCGCTTCCGCGGAGACCCCGC	993
Qy	802	GCACACAGGAACTCTGGCACAATGAGCGCTGCGGTACTGCTGCGCGGTATGGGAG	861
Db	994	GCACACAGGAACTCTGGCACAATGAGCGCTGCGGTACTGCTGCGCGGTATGGGAG	1053
Qy	862	CTAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	921
Db	1054	CTGACGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1113
Qy	922	AGTCCCTGCCAGCACTTGTGCCACCAAGTCCCGCAGAGAACCGCACTGTGATGACCA	981
Db	1114	GACCCCTGCCAGCACTTGTGCCACCAAGTCCCGCAGAGAACCGCACTGTGATGACCA	1173
Qy	982	CAAGATTTCCAGTTGGTGGGAGGCGCACCCCACTCTGCTCCAGGTGAGCACTCGGAG	1041
Db	1174	CTCAGATTTCCCAATTTGCTGAAAGGCGCACCCCACTCTGCTCCAGGTGAGCACTCGGAG	1233
Qy	1042	AAGTTACAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1101
Db	1234	AAGTTACAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1293
Qy	1102	CTGTTAGTGGAGATGAAACCGGCTTCAACACATCATGCTGCTGCTGCTGCTGCTGCTG	1161
Db	1294	CTACTGTTGGAGACAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1353
Qy	1162	GGCTGTACACCACTGCGCGAGATGCGCTTCCAGGAGCTGCTGCTGCTGCTGCTGCTG	1221
Db	1354	GGCTGTACTTCACTACCCAGCAACGCTTCCAGGAGGAGCTGCTGCTGCTGCTGCTGCTG	1413
Qy	1222	CTGCAAGACTTCCGATCAACAGTGTATGAGCTGTGAGAGATGACCAATGGATCG	1281
Db	1414	CTACAGAGCTGAGTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1470
Qy	1282	CTATGGGCTTCCGCGAGTACATCCACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1341
Db	1471	CTATGGGCTTCCGCGAGTACATCCACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1530
Qy	1342	TGCTTACTTGGCTGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1401

Db	1711	CTGTGGAGCCGTCGTGNACTGAGCGGCAGAGGCGCCGCTGGCTTGTGGTTTCA	CGCGACGCG	1770
Qy	1582	CGCCGATATCTGCAGGAGGGTGGCGTGGTAATCTTTCTTCTCGCCGCGCGCGCTGGCG	1641	
Db	1771	CGCCAGACCCTGCAGGAGGCGCGTGGTGGTCTTCTCTCTCCCGGTGGGTGGCG	1830	
Qy	1642	CAGTGTTCAGCAGTGGCTGCA-----CCTCCAGACAGTGGAGCCCGGGCCGCATGAC	1692	
Db	1831	CTGTGTCAGCAGTGGCTACAGATGGGGTGTCTGGGCCCGGGGCGCACGCCCGCACGAC	1890	
Qy	1693	GCCCTCGCGCCTGGCTCAGCTGCGTGCTACTACCGATTTCTGCAAGCCCGGGGACCGCG	1752	
Db	1891	GCCCTCGCGCCTCGCTCAGCTGCGTGTGCTGCCGACTTCTTGCAGGCGCGGGCGCCGGC	1950	
Qy	1753	CGCTACGTGCGGGTCTACTTCGACGCGGCTGCTGCACCCAGACTCTGTGCCCTCCCGGTTTC	1812	
Db	1951	AGCTACGTGGGGGCTGCTTCGACAGGCTGTCTCCACCCGAGTGTCTCCACCGGACGGCGTACCGGCGCTTTTC	2010	
Qy	1813	CGCGTGCGCCCGCTCTTCTCCCTGCCACGACGCTGCGGCTTTTCTGTGANGACTGTGAG	1872	
Db	2011	CGCACCGTGCCTGCTTTCACACTGGCCCTCCCAACTGCCAGACTTCTCTGGGGGCGCTGCAG	2070	
Qy	1873	GGAGGCTGCTCCACTTTCGCGCGGGGGGACCCCGGAGCCGCGTGGNA	1932	
Db	2071	CAGCCTCGCGCCCGCTTCCTGGGCGGCTCCAGAGAGAGCGGAGCAAGTGTCTCCGGGCCC	2130	
Qy	1933	CTGCGGTTCGGCCCTCGGACAGCT-GTACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGGA	1991	
Db	2131	CTTTCAGCCAGCCCTGGATAGCTACTTCATCCCCCGGGGACTCCCGCGCGGGACGCGGG	2190	
Qy	1992	ATGGGACCTGGGAC	2005	
Db	2191	GTGGGACACGSGGC	2204	

RESULT 14	
AEF05348	
ID	AEF05348 standard; cDNA; 2255 BP.
XX	
AC	AEF05348;
XX	
XX	
DT	23-FEB-2006 (first entry)
XX	
DE	Human IL17A and F receptor zcytor14 cDNA SEQ ID NO 1.
XX	
KW	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
KW	antiarthritic; dermatological; antipsoriatic; antibacterial;
KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
KW	inflammatory bowel disease; asthma; respiratory disease;
KW	ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;
KW	gastrointestinal disease; arthritis; antiarthritic;
KW	musculoskeletal disease; psoriasis; antipsoriatic;
KW	dermatological; immune disorder; atopic dermatitis;
KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;
KW	antibacterial; immunosuppressive; infection; zcytor14; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Location/Qualifiers
FT	154..2232
FT	/*tag= a
FT	/product= "zcytor14x1"
FT	214..1509
FT	/*tag= b
FT	/product= "zcytor14x1"
FT	/partial
FT	/note= "No start or stop codon given"
XX	
PN	WO2005123778-A2.
XX	
XX	
PD	29-DEC-2005.
XX	
PP	10-JUN-2005; 2005WO-US2020521.

10-JUN-2004; 2004US-0578805P.
(ZYMO) ZYMOGENETICS INC.
Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
Jaspers SR, Billsborough J;
WPI: 2006-067457/07.
P-PSDB; AEF05349, AEF05350.
New isolated soluble receptor comprises at least one Zcytor14 subunit, useful for treating an inflammatory disease, e.g. asthma, inflammatory bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or psoriasis.
Example 28; SEQ ID NO 1; 205pp; English.
The invention describes an isolated soluble receptor comprises at least one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ ID NO. 24) given in the specification. Also described are: an isolated soluble receptor comprising Zcytor14, where Zcytor14 comprises a polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces the pro-inflammatory activity of either IL-17A comprising fully defined 153 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153 amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2), and where the antibody or antibody fragment reduces the pro-inflammatory activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16); reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal afflicted with an inflammatory disease in which IL-17A or IL-17F plays a role; and treating a pathological condition in a subject associated with Zcytor14 activity. The soluble receptor comprising at least one Zcytor14 subunit is useful for treating an inflammatory disease, e.g. asthma; chronic inflammatory disease selected from inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or psoriasis; or acute inflammatory disease selected from endotoxemia, septicemia, toxic shock syndrome, or infectious disease. This sequence represents human IL-17A and IL-17F receptor zcytor14.
Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;

Query Match	57.5%;	Score 1162.4;	DB 15;	Length 2255;	
Best Local Similarity	75.0%;	Pred. No. 2.1e-246;			5;
Matches 1541;	Conservative 0;	Mismatches 461;	Indels 52;	Gaps	5;

QY	1	ATGCCGTGTCTCGTTCCTCTCTGTCCTTGGCACA	CTGGCCCGAAACCCCTGTGGTCGTCTCT	60
Db	154	ATGCCGTGCGCCTGGTCTTCTGCTTGGCACTGGG	CCGAAACCCAGTGGTCTTCTTCT	213
QY	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGCA	CGCTCTCTTAGGGCTCTCTCTGCCAC	120
Db	214	CTGGAGAGGCTGTGGGGCCTCAGGACGCTACCC	ACTGCTCTTCGGGGCTCTCTCTGCCG	273
QY	121	CTCTGGGATGGTGACGTGCTCTGCTCTGCTGG	AAGCCTCCAGTCTGGCCCGAGGCCCTGTG	180
Db	274	CTCTGGGACAGTGACATATCTTGCCTGCTGGG	ACATGCTGCTCTCGGGCCCCGTG	333
QY	181	CTAGTGCTTACCGGCTGCAGACGGAGCTGGT	GTGCTTGAGGTGCCACAGACAGATTGC	240
Db	334	CTGGCGCCTACGCACCTGCGAGACAGAGCT	TGGTGTCTGAGTGTCCAGAAAGAGACCGACTGT	393
QY	241	GCCTCCGTGTCCGTGTGGTGTGCCATTTGG	CCGTGTCCATTTGGCCGAGAGCCTGAA	300
Db	394	GACCTCTGTCGTGGTGTGCTGTCCACTTTG	CCGTGTCCATTTGGGCACTGGGAAAGAGCCTGAA	453
QY	301	GAAAGCTGGAAAGT-----CTGATTCAGAA	ACTCCAGAGTCTTAGGAAACGGCTCT	348
Db	454	GATGAGGAAAAGTTTGAGAGGAGCAGCTG	ACTCATTAGGGGGTGGAGAGGCTTAGGAATGCTCT	513
QY	349	CTCGAGGCCAGGTGGTGTCTCTTCTCCAGG	CGCTACCCCATCGCCCGCTGTGCCCTCTGCTG	408

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 21:03:24 ; Search time 9736 Seconds
(without alignments)
11613.485 Million cell updates/sec

Title: US-10-719-202-1_COPY_197_2218

Perfect score: 2022

Sequence: 1 atgcctgtctctgttctt.....gacctgcactacactagaa 2022

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST.*

1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_estc.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561.6	77.2	1762	6 AK075634	AK075634 Mus muscu
2	813.8	40.2	1039	1 AV010326	AV010326 AV010326
3	754.2	37.3	850	3 BQ949741	BQ949741 AGENCOURT
4	681.8	33.7	697	2 B1332055	B1332055 602982878
5	668.2	33.0	900	10 DV727885	DV727885 RVL20458
6	643.2	31.8	775	1 A1007139	A1007139 ua81f02.r
7	628.4	31.1	784	2 BG968034	BG968034 602832412
8	620.4	30.7	973	6 AK040950	AK040950 Mus muscu
9	620.4	30.7	3710	6 AK033890	AK033890 Mus muscu
10	612.4	30.3	722	7 BF237179	BF237179 601028133
11	593.8	29.4	597	3 BQ829429	BQ829429 LL6in2310
12	581.2	29.2	643	7 BQ625706	BQ625706 BQ625706
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15	564.4	27.9	847	9 CX756755	CX756755 AGENCOURT
16	562	27.8	562	7 BQ290565	BQ290565 601089427
17	555.8	27.5	1006	7 BQ609618	BQ609618 BQ609618
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21	546.2	27.0	679	3	BQ192107	BQ192107 UI-R-DRI-
22	542.4	26.8	628	3	BP769075	BP769075 BP769075
23	507.8	25.1	1040	3	BQ951730	BQ951730 AGENCOURT
24	503.8	24.9	628	3	BQ210030	BQ210030 UI-R-EP0-
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27	499	24.7	830	9	CX867569	CX867569 HESCA 22
28	498.8	24.7	1060	3	BUS23068	BUS23068 AGENCOURT
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30	477	23.6	609	11	AZ995676	AZ995676 2M0281A07
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33	475.2	23.5	831	5	CK772940	CK772940 961525 MA
34	472.6	23.4	515	5	CJ237410	CJ237410 CJ237410
35	471.6	23.3	499	5	CJ194228	CJ194228 CJ194228
36	464.6	23.0	829	2	BI689749	BI689749 603316255
37	454.4	22.5	787	2	BG917539	BG917539 602817086
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40	444.4	22.0	757	9	CX867488	CX867488 HESCA 22
41	444.2	22.0	771	5	CK774755	CK774755 963540 MA
42	442.6	21.9	932	3	BQ962425	BQ962425 AGENCOURT
43	438.4	21.7	526	2	BI413402	BI413402 602986759
44	436.8	21.6	1086	3	BM920537	BM920537 AGENCOURT
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ALIGNMENTS

RESULT 1	AK075634	1762 bp	linear	HTC 02-SEP-2005
LOCUS	AK075634	Mus musculus 18-day embryo whole body cDNA, RIKEN full-length		
DEFINITION	AK075634	enriched library, clone:110025H02 product:hypothetical protein, full insert sequence.		
ACCESSION	AK075634			
VERSION	AK075634.1	GI:26344438		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1	Carninci, P. and Hayashizaki, Y.		
AUTHORS		High-efficiency full-length cDNA cloning		
TITLE		Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL		10349636		
PUBMED				
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS		Normalization and subtraction of cap-trapper-selected cDNAs to		
TITLE		prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED		11042159		
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kawai, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
AUTHORS		RIKEN integrated sequence analysis (RISA) system--384-format		
TITLE		sequencing pipeline with 384 multicapillary sequencer		
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED		11076861		
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the		
AUTHORS		FANTOM Consortium.		
TITLE		Functional annotation of a full-length mouse cDNA collection		

Db 1026 CATCCACAGCGCTGGTCTTAGTATGGCTGGCTGCTACTCTTGGCTGGCGCTTTT 1085

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Qy 1488 GTTAGAGCAGATGCCACTGCGCTGGCGCTGACCTGTGGAGCCCGCGAGCTGAGCGC 1547

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Db 1446 TTTCTTGAAGCGCGGCGAGCGCGCTAGCTGCGGCTTCTACTTTCGAGCGGCTGCTGCA 1505

Qy 1788 CCAGACTCTGTCCTCCCGTTCCGCTGCGGCTGCGCGCTTCTTCTCCCTGCCACGCGACT 1847

Db 1506 CCAGACTCTGTCCTCCCGTTCCGCTGCGGCTGCGCGCTTCTTCTCCCTGCCCTGCGAGCT 1565

Qy 1848 GCGGCTTCTTCTGATGCACTGACGAGGCTGCTCCTTCCGCGGCGCGACCGCGGA 1907

Db 1566 GCGGCTTCTTCTGATGCACTGACGAGGCTGCTCCTTCCGCGGCGCGACCGCGGA 1625

Qy 1908 CCGGTGGAAAGAGTGAAGCGCGCTGCGGCTGCGGCTTGGACAGCTGCTACTTCTAGCTC 1967

Db 1626 CCGGTGGAAAGAGTGAAGCGCGCTGCGGCTGCGGCTTGGACAGCTGCTACTTCTAGCTC 1685

Qy 1968 GGAAGCCCCAGGCTGCTGCGAGGAATGGAGCTGGGACCTTGCCTACTAGAA 2022

Db 1686 GGAAGCCCCAGGCTGCTGCGAGGAATGGAGCTGGGACCTTGCCTACTAGAA 1740

RESULT 2

AV010326

LOCUS AV010326 Mus musculus 1039 bp mRNA linear EST 23-OCT-2001

DEFINITION clone 1110025H02, mRNA sequence.

ACCESSION AV010326

VERSION AV010326.2 GI:16356130

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Ito, Y., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT On May 11, 1999 this sequence version replaced gi:4787313. Contact: Chie Owa Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@tc.riken.go.jp

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

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10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

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Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

FEATURES

Location/Qualifiers

1..1039

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/db_xref="taxon:10090"

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Best Local Similarity 96.9%; Pred. No. 2.9e-186;

Matches 883; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

Qy 1113 GATCAAAACCGGCTCAACACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACC 1172

Db 112 GAATGAACCGGCTCAACACACATCAGTCTTCTGCG--TTGGAACACGCTGTGTACACA 169

Qy 1173 ACTGCCAGCATGGCTCC-ACGAGAGTGTCTGCTGGGAGAGGAGTGTGTGCAAGACT 1231

Db 170 CTTGCCAGCATGGCTCCAAACGAGAGTGTCTGCTGGGAGAGGAGTGTGTGCAAGACT 229

Qy 1232 TCCGATCACACCACTGTATGAGCTGTGGACGATGACACATGCGATGCGTATGGGCT 1291

Db 230 CCGGATCACACCACTGTATGAGCTGTGGACGATGACACAT-GGATCGCTAT-GGGCT 287

Qy 1292 GCCCATGGACAAGTATACATCACAGGCGCTGGGCTCTAGTATGCTGGCTGCTACTCT 1351

Db 288 GCCCATGGACAAGTATACATCACAGGCGCTGGGCTCTAGTATGCTGGCTGCTACTCT 347

Qy 1352 TGGCTGGGCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1411

Db 348 TGGCTGGGCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 407

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ORIGIN	Query Match Best Local Similarity Matches 822; Conservative	37.3%; 96.4%; 0;	Score 754.2; Pred. No. 8.4e-172; 0;	DB 3; Indels 7; 20;	Length 850; Gaps 5;
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QY	1065	GTGGGTGACTCCTTGGGGCCCTTCAGGATGATATCTGTGTAGTGAGATGAACAACCGG	1124		
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QY	1125	CCTCAACAAACATCAGTCTGTGCTTGTGGAAACCAAGTGGCTGTACACCATGCCCAGCAT	1184		
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QY	1185	GGCTTCCACGAGAGCTGCTGGCTGGGAGGAGTGTCTGCAAGACTTTCGATCACACCA	1244		
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QY	1485	CGCGTTGACCAAGATGCCACTGCGCGTGGCGCTGGACCTGTGGAGCCGCGAGCTGAG	1544		
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DEFINITION	IMAGE:6476411 5', mRNA sequence.					
ACCESSION	BQ949741					
VERSION	BQ949741					
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ORGANISM	Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;						
Sciurognathi; Muridea; Muridae; Murinae; Mus.						
1 (bases 1 to 850)						
NTH-MGC http://mgs.nci.nih.gov/						
National Institutes of Health, Mammalian Gene Collection (MGC)						
Unpublished (1999)						
Contact: Robert Strausberg, Ph.D.						
Email: cgapbs-x@mail.nih.gov						
Tissue Procurement: The Cepko Laboratory						
cDNA Library Preparation: Life Technologies, Inc.						
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)						
DNA sequencing by: Agencourt Bioscience Corporation						
Clone distribution: MGC clone distribution information can be						
found through the I.M.A.G.E. Consortium/LLNL at:						
http://image.llnl.gov						
Plate: LLAMA4016 row: 1 column: 12						
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FEATURES	source					

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ACCESSION BI332055
VERSION    BI332055.1 GI:15016712
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 697)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11333 row: k column: 20
High quality sequence stop: 697.
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                     /clone="IMAGE:5135755"
                     /lab_hosts="NCI CGAP L19"
                     /notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match      33.7%; Score 681.8; DB 2; Length 697;
Best Local Similarity 99.6%; Pred. No. 3.1e-154;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db      1    CAGGAACCTCTGGCACAATAGCCAGGCTGCGGGTACTGTCTCCAGGGGTATGGCAGCTAGA 60
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Db      61    TGGCGCTTGTCTGTCGCGGCAAGGTAAACACTGTGTGTCGAGGCCACCAACAGAGTCC 120
QY      927  CTCGCCAGCCACTTGTGTGCACAGTGCAGGCCAGAGAACGCCACTGTGTGAATGAGCCACAAGA 986
Db      121  CTCGCCAGCCACTTGTGTGCACAGTGCAGGCCAGAGAACGCCACTGTGTGAATGAGCCACAAGA 180
QY      987  TTTTCCA-GTTGGTGGCAGGCCACCCCAACTCTGTGTGTCCAGGTGAGCACCCTGGGAGAAGG 1045
Db      181  TTTTCCATGTTGGTGGCAGGCCACCCCAACTCTGTGTGTCCAGGTGAGCACCCTGGGAGAAGG 240
QY      1046  TTTCACTGCAAGCGTCTGTGTGGGCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGT 1105
Db      241  TTCAGTGCAGCGGTGCTGTGTGGGCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGT 300
QY      1106  TAGTGGAGATGAAACCGGGCTCAACACACATCAGTCTGTGTGCTTGGAAACCCAGTGGCT 1165
|||||
Db      301  TAGTGGAGATGAAACCGGGCTCAACACACATCAGTCTGTGTGCTTGGAAACCCAGTGGCT 360
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QY      1226  AAGACTTCCGATCACACACAGTGTATGACGTGTGGACGATGACACATGGGATCGCTAT 1285
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QY      1286  GGGCTGCGCCCATGGAACAAAGTACATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCC 1345
Db      481  GGGCTGCGCCCATGGAACAAAGTACATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCC 540
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LOCUS      RVL20458 Wackym-Soares normalized rat vestibular cDNA library
DEFINITION Rattus norvegicus cDNA 5', mRNA sequence.
ACCESSION DV727885
VERSION    DV727885.1 GI:82521209
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 900)
Wackym, P.A., Erbe, C.B., Samuels, T.L., Eernisse, R.R., Popper, P.,
Cioffi, J.A. and Wittek, A.E.
Analysis of 20,000 Clones from a Normalized Rat Vestibular cDNA
Library
Unpublished (2006)
Contact: Wackym, P.A.
Department of Otolaryngology and Communication Sciences
9200 W. Wisconsin Ave, Milwaukee, WI, 53226, USA
Tel: 414.266.3750
Fax: 414.266.2693
Email: wackym@mcw.edu
Insert Length: 900 Std Error: 0.00
Seq primer: T7.
FEATURES             Location/Qualifiers
     source           1..900
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                     library"
                     /notes="Vector: pT73Pac; The library was constructed and
                     normalized according to Bonaldo and Soares, Genome Analysis -
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                     directionally cloned into the EcoRI and NotI sites. The
                     library tag located between the NotI site and the polyA
                     tail is TAGGTACAC."
ORIGIN
Query Match      33.0%; Score 668.2; DB 10; Length 900;
Best Local Similarity 85.1%; Pred. No. 6.5e-151;

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prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

REFERENCE	Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636	FEATURES	source 1..973 Location/Qualifiers /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:A530050M19" /db_xref="taxon:10090" /clone="A530050M19" /sex="male" /tissue_type="aorta and vein" /tissue_lib="RIKEN full-length enriched mouse cDNA library" /clone_lib="adult" /dev_stage="adult"	misc_feature 1..973 /note="putative unclassifiable"
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159	ORIGIN	Query Match 30.7%; Score 620.4; DB 6; Length 973; Best Local Similarity 99.8%; Pred. No. 2.6e-139; Matches 621; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1401 AGCGGCGCGTGGCTCCCGCACGGCTTGTCTCCCTCCACTCCGCGCGGCGGTACGA 1460 Db 670 AGCGGCGCGTGGCTCCCGCACGGCTTGTCTCCCTCCACTCCGCGCGGCGGTACGA 611 QY 1461 GCGTCTGGTGGAGCACTGGCGTTCGGCTGTAGCCAGATGCCACTGCGCGTGGCGTGA 1520 Db 610 GCGTCTGGTGGAGCACTGGCGTTCGGCTGTAGCCAGATGCCACTGCGCGTGGCGTGA 551 QY 1521 CCGTGTGAGCGCGCGGAGCTGAGCGCGCACGAGCGCTTAGCTGGTTCACACACGCG 1580 Db 550 CCGTGTGAGCGCGCGGAGCTGAGCGCGCACGAGCGCTTAGCTGGTTCACACACGCG 491 QY 1581 AGCGCGTATCTCGAGAGGGTGGCGTGTGTATCTTCTTCTTCTGCGCGCGCGTGGC 1640 Db 490 AGCGCGTATCTCGAGAGGGTGGCGTGTGTATCTTCTTCTTCTTCTGCGCGCGCGTGGC 431 QY 1641 GCAGTGTACAGTGGCTGCGAGCTCCAGACAGTGGAGCGCGCGCGCGCATGACGCGCTCGC 1700 Db 430 GCAGTGTACAGTGGCTGCGAGCTCCAGACAGTGGAGCGCGCGCGCGCATGACGCGCTCGC 371 QY 1701 CGCTGTGCTCAGTGGCTGCTGCTACCCGATTTCTTCCAGAGCGCGCGCGCGCTACGT 1760 Db 370 CGCTGTGCTCAGTGGCTGCTGCTACCCGATTTCTTCCAGAGCGCGCGCGCGCTACGT 311 QY 1761 CGGGGTCTACTTTCGACGGGCTGCTGACCCAGAGCTCTGTGCGCTTCCCGCTCGCGTGC 1820 Db 310 CGGGGTCTACTTTCGACGGGCTGCTGACCCAGAGCTCTGTGCGCTTCCCGCTCGCGTGC 251 QY 1821 CCGGCTCTTCTCCCTGCGCACGAGTGGCGGCTTCTCTGGATGCACTGCAAGGAGGCTG 1880 Db 250 CCGGCTCTTCTCTCCCTGCGCACGAGTGGCGGCTTCTCTGGATGCACTGCAAGGAGGCTG 191 QY 1881 CTCGATTTCCGCGGGGCGACCCCGCGGACCGCGGTGGAACGAGTACCCAGGCGCTCGGTC 1940 Db 190 CTCGATTTCCGCGGGGCGACCCCGCGGACCCCGGTGGAACGAGTACCCAGGCGCTCGGTC 131 QY 1941 CGCGCTTGACAGCTGACTTCTAGCTCGGAAGCCCGAGGCTCTCTGCGAGGAATGGGACT 2000 Db 130 CGCGCTTGACAGCTGACTTCTAGCTCGGAAGCCCGAGGCTCTCTGCGAGGAATGGGACT 71 QY 2001 GGGACCTGCACTACACTAGAA 2022 Db 70 GGGACCTGCACTACACTAGAA 49	
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861	RESULT 9 AK033890/c LOCUS		
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)			
REFERENCE	The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)			
REFERENCE	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)			
REFERENCE	The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)			
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
TITLE	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to			
COMMENT				

DEFINITION	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330110N14 product:unclassified, full insert sequence.
ACCESSION	AK033890
VERSION	AK033890.1 GI:26083639
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBMED	
REFERENCE	
AUTHORS	The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	
REFERENCE	
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE	Antisense Transcription in the Mammalian Transcriptome
JOURNAL	Science 309, 1564-1566 (2005)
PUBMED	
REFERENCE	
AUTHORS	The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE	The Transcriptional Landscape of the Mammalian Genome
JOURNAL	Science 309, 1559-1563 (2005)
PUBMED	
REFERENCE	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saichoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

QY	2001	GGGACCCCTGCATCTACACTAGAA	2022
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VERSION	EST.		
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs-re@mail.nih.gov Tissue procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Cloned through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9447 row: a column: 10 High quality sequence stop: 594.		
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/lab_host="DH10B (T1 phage-resistant)"			
/clone_lib="NCI CGAP L19"			
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."			
ORIGIN			
Query Match	30.3%	Score 612.4;	DB 7; Length 722;
Best Local Similarity	99.0%	Pred. No. 2.2e-137;	
Matches 616;	Conservative 0;	Mismatches 6;	Indels 0; Gaps 0;
QY	1401	AGCGGCCCGGTGCGCAGCGCTTGCTTCCTCCACTCCGCGGACGAGCGGGGTACGA	1460
Db	630	AGCGGCGGTGGCTCCCGCACGACCTGGCTCTCCGCTCCGCGGACGAGCGGGGTACGA	571
QY	1461	GCGTCTGGTGGAGCACTGCGCTCCGCTTGAGCAGATGCCACTGCGCGTGGCGGTGGA	1520
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QY	1521	CCTGTGGAGCCGCGCGAGCTGAGCGGCGACGAGCCCTAGCTGTTCCACCACGAGCG	1580
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QY	1581	ACGCCGTATCTGCAGGAGGTGGCTGTAATCTTCTCTCTCCGCGCGCGGTGGC	1640
Db	450	ACGCCGTATCTGCAGGAGGTGGCTGTAATCTTCTCTCTCCGCGCGCGGTGGC	391
QY	1641	GCAGTGTTCAGCAGTGGCTGCAGCTCCAGACGTGAGCCCGGCGCGCATGACGCCCTCGC	1700
Db	390	GCAGTGTTCAGCAGTGGCTGCAGCTCCAGACGTGAGCCCGGCGCGCATGACGCCCTCGC	331
QY	1701	CGCTGGCTCAGCTGGTGTACCCGATTCTCTGCAAGCCGCGGCGGACCGCGCGCTACGT	1760

stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, 2018 cDNA library in pSport2 with inserts cloned in the complementary orientation. The Afr2024-subtracted library contains 4.2x10⁵ clones and is depleted of common housekeeping gene products eg. beta-actin and enriched for transcripts specific to Afr2024. For detailed protocols and additional information please see our website at <http://stromalcell.princeton.edu>."

ORIGIN

Query Match	29.4%;	Score 593.8;	DB 3;	Length 597;
Best Local Similarity	99.7%;	Pred. No. 7.1e-133;		
Matches 595;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	807	CAGGAACCTCTGGCACA	TAGCAGCGCTGCGGGTACTGTCC	CAGGGGTATGGCAGCTAGA 866
DB	1	CAGGAACCTCTGGCACA	TAGCAGCGCTGCGGGTACTGTCC	CAGGGGTATGGCAGCTAGA 60
QY	867	TGCGCTTGTCTGTCTGCCGGGCA	AGTTAACTGTGTCTGCGCAGGCA	CCACAGACGAGTCC 926
DB	61	TGCGCTTGTCTGTCTGCCGGGCA	AGTTAACTGTGTCTGCGCAGGCA	CCACAGACGAGTCC 120
QY	927	CTGCCAGACCACTTGTGCCAC	CAGTGCCTCCAGAGAGCGCCAC	TGTCGAATGAGCCACAGA 986
DB	121	CTGCCAGACCACTTGTGCCAC	CAGTGCCTCCAGAGAGCGCCAC	TGTCGAATGAGCCACAGA 180
QY	987	TTTTCCAGTTGGTGGCAGGSC	CAACCCCACTCTGTCTCCAGGT	GAGCACCTGGGAGAAAGT 104
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QY	1167	TACACCACTGCCAGCATGCGCT	CCAAGAGAGTCTGCGCTGGGAG	AGGAGTTGCTGCA 1226
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QY	1227	AGACTTCCGATCACACAGTGT	ATGCGAGCTGTGGACGATGAC	CAATGGGATCCGTATG 1288
DB	421	AGACTTCCGATCACACAGTGT	ATGCGAGCTGTGGACGATGAC	CAATGGGATCCGTATG 480
QY	1287	GGCCTGCCCCATGGAACAAGT	TACATCCACAGCGCTGGGTCT	TAGTATGCTGGCCTGCT 1346
DB	481	GGCCTGCCCCATGGAACAAGT	TACATCCACAGCGCTGGGTCT	TAGTATGCTGGCCTGCT 540
QY	1347	ACTCTTGCTCGGGCGCTTTTCT	TCTTCCTTTCTTAAAAAAGG	ACCGCAGGAAAGC 1403
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[illegible]

Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, K., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Itoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Havaishizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001). Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
SOURCE

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1. 643
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mol_type="nrna"
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diencephalon".

/note=Site1: Sali; Site_2: BamHI; cDNA library was prepared and sold in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGCATCAGAGCTCTTTTTTTTTTTTWN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTGTAATAATATACCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIC I. Cloning sites, 5' end: Sali; 3' end: BamHI".

ORIGIN

Query Match

29.2%; Score 591.2; DB 7; Length 643;

Fax: 81-45-503-9216
Email: genome-resesc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
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Computer-based methods for the mouse full-length cDNA
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Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTATTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

ORIGIN

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DB 620 GAGCGGCTACGAGCGTCTGGTGGAGCACTGGCTCCGGTGGAGCAGATGCCACTGC 561

QY 1508 GCGTGGCGGTGACCTCTGGAGCGCGCGAGCTGAGCGCGACGAGCGCTAGCTGGT 1567

DB 560 GCGTGGCGGTGACCTCTGGAGCGCGCGAGCTGAGCGCGACGAGCGCTAGCTGGT 501

QY 1568 TCCACCAACGAGCGCGGTATCTCGAGAGGGTGGCGTGAATCCTTCTCTTCGCG 1627

DB 500 TCCACCAACGAGCGCGGTATCTCGAGAGGGTGGCGTGAATCCTTCTCTTCGCG 441

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REFERENCE	1 (bases 1 to 847)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Meri Firpo cDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI5907 row: 9 column: 20 High quality sequence start: 15 High quality sequence stop: 759. Location/Qualifiers			
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	/clone_lib="NIH_MGC_278"			
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ORIGIN				
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QY	121	CTCTGGATGGTGCACGTGTCTCTGCTGCTCTGGAAGCCTCCAGTCTGTGCCCGCCCTGTG	180	
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3	62	3.1	4076	3	Sequence 4839, Ap
4	62	3.1	4163	3	Sequence 748, App
5	62	3.1	12438	3	Sequence 1581, A
6	62	3.1	16321	3	Sequence 12490, A
7	54	2.7	7950	3	Sequence 934, App
8	51.4	2.5	5430	4	Sequence 31, Appl
9	50	2.5	4563	3	Sequence 259, App
10	50	2.5	4563	3	Sequence 259, App
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	Prior Application Number	US 60/242,837						
	Prior Filing Date	2000-10-24						
	Prior Application Number	PCT/US00/30873						
	Prior Filing Date	2000-11-10						
	Prior Application Number	US 60/253,646						
	Prior Filing Date	2000-11-28						
	Prior Application Number	PCT/US00/32678						
	Prior Filing Date	2000-12-01						
	Number of Seq ID NOS	39						
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	US-09-747-259-13							

	Prior Application Number	US 09/644,848	Query Match	55.1%	Score 1113.4	DB 3	Length 2380	
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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
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Thu Aug 17 14:34:40 2006

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QY 1977 AGCTGTGCGAGGATGGGACCTGGAC 2005
Db 2539 GCGCGGCGCGCGGTGGGACCGAGGGC 2567

RESULT 3
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; Sequence 4839, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4839
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4839

Query Match 3.1%; Score 62; DB 3; Length 4076;
Best Local Similarity 47.2%; Pred. No. 2.9e-05;
Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 1463 GTCTGTGGGAGCACTGGCGTTCGCGGTGAGCCAGATGCCACTGCGCGTGGCGCGTGGAC 1522
Db 1443 GCGTGGAGTGGCCACGCGGCGCTTGGAGGCGCTTGGAGGCTCTCTTGGAGTCTTGGCAC 1502
QY 1523 TGTGGAGCGCGCGAGCTGAGCGCGCACGGAGCCCTAGCCTGTGTTCCACACAGCGAC 1582
Db 1503 TGCAGGGCAACCGGCTGATGGTGTCTGACGAGTGTGAGCCACTTCCCGCGCTGACCT 1646
QY 1583 GCGGTATCTCTGAGGAGGTGGGTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1642
Db 1647 GCGTCAATCTTCCGAGAGAACCGCTGAGCCACTTCCCGCGCTGAGCACAGGCTGTGTAC 1706
QY 1643 AGTGTGAGAGTGGCTGAGCTTCCAGACAGTGGAGCCCGGCGCGCATGACGCGCTCGCG 1702
Db 1707 TGGAGGTGTGAGCTTCCGAGAACACAGCTTCCAGCGCTTCCGCGCGCATGAGTGGGTG 1766
QY 1703 CCTGGGTGAGCTGCTGCTACCGATTTCTTGAAGCGCGGCGACCGCGCTAGCTG 1762
Db 1767 GCGTGGAGACGAGCTTCCGCGCGCTTCTTCTGAGGGGAATCCACTGAGTGTCTGGCA 1826
QY 1763 GGGTCTACTTCTGAGCGGCTGCTGACCGAGCTTCTGTGCGCTTCCCGGTTCGCGTCC 1822

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QY 1583 GCGGTATCTCTGAGAGGCTGGGTGTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1642
Db 1563 GCGTCAATCTTTCGCCAGAACCGCTGAGCCACTTTCGCCGTGAGACACAGGCTGTGTAC 1622
QY 1643 AGTGTGAGAGTGGCTGAGCTTCCAGACAGTGGAGCCCGGCGCGCATGACGCGCTCGCG 1702
Db 1623 TGGAGTGTGAGCTTCCGAGAACACAGCTTCCAGCGCTTCTGCGAGGAGTGGCATGGGTG 1682
QY 1703 CCTGGCTGAGCTGCTGCTACCGATTTCTTGAAGCGCGGCGACCGCGCTAGCTG 1762
Db 1683 GCGTGGAGACGAGCTTCCGCGCGCTTCTTCTGAGGGGAATCCACTGAGTGTCTGGCA 1742
QY 1763 GGGTCTACTTCCAGCGGCTGCTGACCGAGCTTCTGTGCGCTTCCCGGTTCGCGTCC 1822
Db 1743 ATGGCTGGCTGGAGCGCGCTGACCGAGGCTGACCGAGGCGGTGTGAGCGCGCACCCAGG 1802
QY 1823 CGCTCTTCTCTTCCGCGCGCTGAGCTGCGCGGCTTCTCTG 1860
Db 1803 TGAATCTGCGCTTCACTGCTCCAGGAGGAGTGTGCTCTG 1840

RESULT 4
US-09-949-016-748
; Sequence 748, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-748

Query Match 3.1%; Score 62; DB 3; Length 4163;
Best Local Similarity 47.2%; Pred. No. 2.9e-05;
Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 1463 GTCTGTGGGAGCACTGGCGTTCGCGGTGAGCCAGATGCCACTGCGCGTGGCGCGTGGAC 1522
Db 1527 GCGTGGAGTGGCCACGCGGCGCTTGGAGGCGCTTGGAGGCTCTTCTTGGAGTCTTGGCAC 1586
QY 1523 TGTGGAGCGCGCGAGCTGAGCGCGCACGGAGCCCTAGCCTGTGTTCCACACAGCGAC 1582
Db 1587 TGCAGGGCAACCGGCTGATGGTGTCTGACGAGTGTGAGCCACTTCCCGCGCTGACCT 1646
QY 1583 GCGGTATCTCTGAGGAGGTGGGTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1642
Db 1647 GCGTCAATCTTCCGAGAGAACCGCTGAGCCACTTCCCGCGCTGAGCACAGGCTGTGTAC 1706
QY 1643 AGTGTGAGAGTGGCTGAGCTTCCAGACAGTGGAGCCCGGCGCGCATGACGCGCTCGCG 1702
Db 1707 TGGAGGTGTGAGCTTCCGAGAACACAGCTTCCAGCGCTTCCGCGCGCATGAGTGGGTG 1766
QY 1703 CCTGGGTGAGCTGCTGCTACCGATTTCTTGAAGCGCGGCGACCGCGCTAGCTG 1762
Db 1767 GCGTGGAGACGAGCTTCCGCGCGCTTCTTCTGAGGGGAATCCACTGAGTGTCTGGCA 1826
QY 1763 GGGTCTACTTCTGAGCGGCTGCTGACCGAGCTTCTGTGCGCTTCCCGGTTCGCGTCC 1822

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Db 1827 ATGGCTGGCTGGCAGCCAGCTGCACACAGGGCGGTGTGGACGTGGACGCCACCCAGGACC 1886

Qy 1823 CGCTCTTCTCCCTGCCACGACGAGCTGCCGGCTTTCCCTG 1860
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 Db 1887 TGAATCTGCGCTTCAGCTCCACGAGGAGGTTGTCCCTG 1924
 |||||

RESULT 5

US-09-949-016-16581

; Sequence 16581, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16581

; LENGTH: 12438

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-16581

Query Match 3.1%; Score 62; DB 3; Length 12438;

Best Local Similarity 47.2%; Pred. No. 4.2e-05;

Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

Qy 1463 GTCTGTGGGAGACACTGCGCTCCGGCTTTGAGCAGATGCACATGCGCGTGGCCGTGGACC 1522
 |||||
 Db 7805 GCCTGGAGGTGGCCACCGGGGCTTTGGGAGGCGCTTGGAGGCTCTTGGAGGTTCTTGGCAC 7864

Qy 1523 TGTGAGCGCGCGAGCTGAGCGCGCAGGAGCCCTAGCTTGTTCCACACCCAGCGAC 1582
 |||||
 Db 7865 TGCAGGGCAACGGGCTGATGTCTTCGAGGTGGACCTGCCCTGTTCATCTGCCTCAAAGC 7924

Qy 1583 GCCGTATCTCTCAGGAGGTGGCGTGTGAATCTTCTCTTCGCGCGCGCGCGTGGGCG 1642
 |||||
 Db 7925 GGCTCAATCTTCCGAGAACCGCTTAGCCACCTTCCGCGCTTGACACAGGCTGTGTAC 7984

Qy 1643 AGTGTACAGCAGTGGCTGCAGCTCCACAGAGTGGAGCCCGGGCGCGATGACGCCCTCGCG 1702
 |||||
 Db 7985 TGGAGGTGCTGACCTGCGAACAACAGCTTCAGCTCTCTGCAGGAGTGCATGGGTG 8044

Qy 1703 CTTGGCTCAGTGGCTGTATCCGATTTCTGCAAGCGCGGGCGAGCCGCGCTACGTGG 1762
 |||||
 Db 8045 GCCTGGAGACAGCCTCCGGGCGCTCTACCTGCAAGGGAATCACTCAGCTGTCTGCGGCA 8104

Qy 1763 GGGTCTACTTTCAGCGGGCTGTGCACCCAGACTCTGTGCCCTCCCGTTCCGCGTCCGCC 1822
 |||||
 Db 8105 ATGGCTGGCTGGAGCCAGCTGCACACAGGCGGTGTGACGTGAGACGCCACCCAGGACC 8164

Qy 1823 CGCTCTTCTCCCTGCCACGAGCTGCCGGCTTTCCCTG 1860
 |||||
 Db 8165 TGAATCTGCGCTTCAGCTCCACGAGGAGGTTGTCCCTG 8202
 |||||

RESULT 6

US-09-949-016-12490

; Sequence 12490, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Thu Aug 17 14:34:40 2006

ORGANISM: Myxococcus xanthus
US-09-902-540-934
Query Match 2.7%; Score 54; DB 3; Length 7950;
Best Local Similarity 44.7%; Pred. No. 0.0034;
Matches 253; Conservative 0; Mismatches 310; Indels 3; Gaps 1;
QY 1427 TGCTCTCCACTCCGCGCGAGCGGCTACAGAGCGCTGTGGTGGAGCACTGGCGTCCG 1486
Db TGGCCAGCACCTGCATACGAGCGCTCCACGTCGCGCAGTAACGGCGCACTGCGGT 2866
QY 1487 CATTGAGCGAGTGCATCTGCGTGGCGGACCTGTGGAGCGCGCGAGCTGAGCG 1546
Db CGTCTCTCGGAGCAGAAAGATGGGGTAGCCACAGTTGGCGGGCCATGTTAGTG 2926
QY 1547 CGCAGGAGCCCTAGCTGTGTTCCACCAAGCGAGCGCGTATCTTGAGGAGGGTGGG 1606
Db AGTGTGCGCCACGCTGTGTTCTCGAAGACCTTCGCGCCCTCTTCGCCAATGCGCGTGC 2986
QY 1607 TGGTAATCTCTTCTGCGCGCGCGGTGGCGAGTGCAGTGGCTGCAGCTCC 1666
Db CTGGGACGATGTTCTACGCTTCGCGGACCGGCCAGGTGAGATGGCGGGTGTCTCC 3046
QY 1667 AGACAGTGAGCGCGGCGCGATGACGCGCTCGCGCTGCGCGCGACTCGCTGAAGAGGTGCATC 3106
Db AGAGAGAGCAGACATCGCGGAGAGCCCTTCGCGCGCGACTCGCTGAAGAGGTGCATC 3106
QY 1727 ATTTCCTGCAAGCGCGGCGACGCGCGTACGTGCGGGTCTACTTCGACGGGCTGTGC 1786
Db AGCGGAGCGCGCTCTCGTACTCCACTCGCGCCGAGCGGTAGACGGTATGTTGTCATG 3166
QY 1787 ACCGAGCTGTGCGCTCCCGTTCGCGGTGCGCGCTCTTCTTCCTTCGCGCGAGC 1846
Db ACCTGCTCTCTTTCGAGCC--TTTCGCGTGGCGAGGGCTTCACGGTGGCGCGCAGGC 3223
QY 1847 TGCGCGCTTTCCTGGATGCACTGAGGAGGCTGCTCCACTTCGCGGGGCGACCGCGG 1906
Db TCCACGTTCCCGTGGGTACCGGTTGAGGAGGCGATGCACTGCGCGCGCGCGCGG 3283
QY 1907 ACCGGTGGACGAGTACCGAGCGCTGCGGTCCGCGCTTCGAGACGCTGTACTTTAGCT 1966
Db AGCGGCTGGGCTCTCGGCGAGCGCCATGACACTTCTTCGAGAGCGGAGACCGCGGCT 3343
QY 1967 CGGAAGCGCCAGGCTGTGCGAGAA 1992
Db CTCGAGGCGCAGGCGCTGGCGGCA 3369

RESULT 8
US-10-324-967-31
; Sequence 31, Application US/10324967
; Patent No. 6974680
; GENERAL INFORMATION:
; APPLICANT: Cosson, Pierre
; APPLICANT: Kohler, Thilo
; APPLICANT: Benghezal, Mohammed
; APPLICANT: Marchetti, Anna
; APPLICANT: van Deiden, Christian
; TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE
; FILE REFERENCE: 25421-502
; CURRENT APPLICATION NUMBER: US/10/324,967
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 31
; LENGTH: 5430
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-324-967-31
Query Match 2.5%; Score 51.4; DB 4; Length 5430;
Best Local Similarity 47.1%; Pred. No. 0.013;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
QY 1403 CGCGCGGTGGCTCCGCGAGCGCTTGTCTCTCCACTCCCGCCGAGCGGCTACGAGC 1462
Db 485 CGCGCGGTCTCG 426
QY 1463 GTCTGGTGGAGC-ACTGGCGTCCCGGTTGAGCAGATGCCACTGCGCGTGGCGGAC 1521
Db 425 GCGCTAGCGCGGTGCG 366

RESULT 9
US-10-012-231A-259/c
; Sequence 259, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-012-231A-259
Query Match 2.5%; Score 50; DB 3; Length 4563;
Best Local Similarity 45.5%; Pred. No. 0.027;
Matches 214; Conservative 0; Mismatches 255; Indels 1; Gaps 1;
QY 1403 CGCGCGGTGGCTCCGCGAGCGCTTGTCTCTCCACTCCCGCCGAGCGGCTACGAGC 1462
Db 485 CGCGCGGTCTCG 426
QY 1463 GTCTGGTGGAGC-ACTGGCGTCCCGGTTGAGCAGATGCCACTGCGCGTGGCGGAC 1521
Db 425 GCGCTAGCGCGGTGCG 366

Qy	1522	CTGTGTGAGACCGCCCGCGAGCTGAGCGCGCA	CGAGCGCTTACGCTGTGTTCAACCAACGCA	1581
Db	365	CCCGGGCAGCGCCCGCGCGCGCGCGCCATCGCGGCCCCCGACGCGCCC	306	
Qy	1582	CGCCGTATCTCTGCAGAGAGGGTGGCGTGTGTAATCTTCTTCTTCTCGCCCGCGGCGCTGGCG	1641	
Db	305	CGAGGCCCGCGCGCGCTTTGTTCGCA	CACCCGCCCCCGCGCGCTGGCGCCT	246
Qy	1642	CAGTGTGAGCAGTGGCTGCAGCTCCAGACAGTGGAGCCCGGGCGCATGAGCGCTTCGCC	1701	
Db	245	TTAAGAGGGACCATGCCCCGCGCGCTACGCGCGCTCTCGGGCGCGAGTGGCGGCGGC	186	
Qy	1702	GCCTGGCTCAGCTGCGTCTACCCGATTTCTTCAAGCGCGGGCGACCGCCGCTACGTC	1761	
Db	185	TCCTCCGCTCGCGCGGGGAGCGCGGGCGCGCA	CGACGCGACGCGCGCGGCGAGA	126
Qy	1762	GGGTCTTACTTCGAGAGGGCTGCTGCA	CCCGAGACTCTGTGCGCTCCCGTTCCGGTTCGCC	1821
Db	125	CGAGTCGGGGTCCCGTCCCGCTCCCGGTCTCCGGCTGGCTGGGCTCGGTTGCGCA	66	
Qy	1822	CCGCTCTTCTCCCTGCCCCACGCA	CGAGCTCCCGCTTTCCTGGATGCATGCA	1871
Db	65	CGGCGCTGTCTCCCGTCTCTTTCGTAGCCGCGCGCGCGCGCAGCTGCA	16	

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RESULT 10
US-10-015-389A-259/c
; Sequence 259, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Saton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACID ENCODING: Acids Encoding the Same
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
; US-10-015-389A-259

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	Query Match	2.5%	Score 50;	DB 3;	Length 4563;
	Best Local Similarity	45.5%;	Pred. No. 0.027;		
	Matches 214;	Conservative 0;	Mismatches 255;	Indels 1;	Gaps 1;
Qy	1403	CGGCCCGTGCTCCGACGCGCTTGCTCTCCATCCGCGCAGCGAGCGGGCTACGAGC	1462		
Db	485	CGCGCCGCTCGCGCCGCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	426		
Qy	1463	GTCTGTGGGAGC-ACTGGGCGTCGGCGTTAGCGACAGATGCCATGTGCGCTGGCGCTGGAC	1521		
Db	425	GCCTCAGCCCGGTGCCCGCCGCCACAGAGGCCAGCCCGCTTATGGCGCGCGAGGCCCGG	366		

Qy	1522	CTGTGGAGCCGCGCGAGCTGAGGGCGACGAGAGCCCTAGCTGGTTTCCACCAACGACGA	1581
Db	365	CCCGGGCAGCGCGCGCGCGCGCGCGCGCGCGCCATCGCGGCCCCCGAGCGCGCC	306
Qy	1582	CGCGGTATCTCTGAGAGGGTGGCGTGTAACTCTTCTTCTTCGCGCGCGGGCGGTGGCG	1641
Db	305	GCAGGCCCGCGCGCGGCTTGTTCGCGACACCCGCCCCCGCGCGCGGCTCGGCCT	246
Qy	1642	CAGTGTCAAGATGGCTGCAGCTTCAGATGGAGCCCGGGCCGATGACGCCCTCGCC	1701
Db	245	TTAAGAGGGACCATGCCCGCGCGCGCTAGCGCGGCTCGGGCGCGAGTGGCGCGCGC	186
Qy	1702	GCCTGGCTCAGCTGCGTGTACTCCGATTTCTCTCAAGGCGCGGCGGACCGGCCCTACGTC	1761
Db	185	TCCTCCGCTCGCGCGGGGACCGGGGCGGCACAGCGGCGACGACGGCGCGCGAGA	156
Qy	1762	GGGGTCTACTTCAGAGGGCTGTGCACCCAGACTCTGTGCCCTCCCGTTCGCGGTGCGC	1821
Db	125	CGAGTTCGGGCTCCCGTCCCGCCCTCCCGCGTCTCCGGCTGGCTGGGGCTCGGTTGCGA	66
Qy	1822	CCGCTCTTCTCCCTGCCACGCGAGCTGCCGGCTTTCTCGATGCACTGCA	1871
Db	65	CGCGGCTGTGTCGGTCTCTTCGTAGCGGGGCGCGCGCGAGCTGCA	16

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RESULT 11
US-10-006-768A-259/c
; Sequence 259, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   ACIDS ENCODING THE SAME
; FILE REFERENCE: P2830PIC10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-006-768A-259

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[illegible]

QY	1522	CTGTGGAGCGCGCGAGCTGAGCGCGCACGAGAGCCCTAGCCTGGTTCCACCAACGCGA	1581
Db	365	CCCGGGCAGCGCGCGCGCCCGCGGCGCCATCGCGGCCCCCGAGCGCCCC	306
QY	1582	CGCGGTATCTCTGAGAGGGGTGGCGTGAATCCTTCTTCTCGCCCGCGCGCTGGCG	1641
Db	305	GCAGGCCCCCGCGCGCGCTTTGTTCGCAACACCGGCCCGCGCGCTGCGCCT	246
QY	1642	CAGTGTGAGCAGTGGCTGCACTCCAGACAGTGGAGCCCGGGCGCGCATGACGCCCTCGCC	1701
Db	245	TTAAGAGGGACCATGCTCCGCGCGCGCTAGCGCGCTCGGCGCGCAGGTGGCGCGCG	186
QY	1702	GCTTGGCTCAGCTGCGTGTCTACCGATTTCTGCAAGCGCGGGCGACCGGCCGTACGTC	1761
Db	185	TCCTCCCGCTCGCGCGCGGGACCGGGGCGGACGACGCGACGACGGCGCGGAGAGA	126
QY	1762	GGGGTCTACTTCGACGGGCTGTCTGCACCCAGACTCTGTGCCCCCTCCCGTTCCGCGTCCGC	1821
Db	125	CGAGTCGGGGTCCCGTCCCGCTCCCGGTCTCTCGGCTGGCTGGGCTTCGCA	66
QY	1822	CCGCTCTTCTCCCTGCCCAACGACGATGCGCGGCTTTCTTGGATGACATGCA	1871
Db	65	CGGCGCTGTCCCGTCTCTTCGTAGCGCGCGCGCGCGCGACAGTCA	16

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RESULT 12
US-10-015-671A-259/c
; Sequence 259, Application US/10015671A
; Patent NO. 6946263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Scrsted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-015-671A-259

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[illegible]

[illegible]

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 09:07:13 ; Search time 2082 Seconds
(without alignments)
5966.762 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

Sequence: 1 MPVSWFLSLALGRNPVWS.....SSBAPGCCCEWDLGPTTILE 674

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
-USER=US10719202 @CGN_1_1675 @runat_16082006_095638_13381 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10K_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	3605	100.0	2256	3 US-09-899-471-1

2	3605	100.0	2256	8	US-10-719-202-1	Sequence 1, Appli
3	3583	99.4	2328	3	US-09-899-471-4	Sequence 4, Appli
4	3583	99.4	2328	8	US-10-719-202-4	Sequence 4, Appli
5	3572.5	99.1	2269	16	US-11-150-533-25	Sequence 25, Appli
6	3569.5	99.0	2287	16	US-11-150-533-29	Sequence 29, Appli
7	3565	98.9	2314	3	US-09-863-618A-7	Sequence 7, Appli
8	3565	98.9	2314	9	US-10-749-144-7	Sequence 7, Appli
9	3565	98.9	2314	9	US-10-924-667-7	Sequence 7, Appli
10	3562	98.8	2128	3	US-09-866-050A-487	Sequence 487, App
11	3562	98.8	2128	6	US-10-152-661-487	Sequence 487, App
12	3539	98.2	2331	8	US-10-416-442A-74	Sequence 74, Appli
13	2666	74.0	2022	3	US-09-899-471-3	Sequence 3, Appli
14	2666	74.0	2022	8	US-10-719-202-3	Sequence 3, Appli
15	2644	73.3	2094	3	US-09-899-471-6	Sequence 6, Appli
16	2644	73.3	2094	8	US-10-719-202-6	Sequence 6, Appli
17	2352.5	65.3	2255	7	US-10-458-647-1	Sequence 1, Appli
18	2352.5	65.3	2255	16	US-11-150-533-1	Sequence 1, Appli
19	2339	64.9	2380	3	US-09-874-503-13	Sequence 13, Appli
20	2339	64.9	2380	3	US-09-747-259-13	Sequence 13, Appli
21	2339	64.9	2380	3	US-09-908-827-13	Sequence 13, Appli
22	2339	64.9	2380	6	US-10-006-867-161	Sequence 161, App
23	2339	64.9	2380	6	US-10-052-586-597	Sequence 597, App
24	2339	64.9	2380	6	US-10-063-547-161	Sequence 161, App
25	2339	64.9	2380	6	US-10-000-157-13	Sequence 13, Appli
26	2339	64.9	2380	6	US-10-063-551-161	Sequence 161, App
27	2339	64.9	2380	6	US-10-174-590-597	Sequence 597, App
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42	2339	64.9	2380	6	US-10-175-752-597	Sequence 597, App
43	2339	64.9	2380	6	US-10-176-482-597	Sequence 597, App
44	2339	64.9	2380	6	US-10-176-757-597	Sequence 597, App
45	2339	64.9	2380	6	US-10-176-913-597	Sequence 597, App

ALIGNMENTS

RESULT 1
US-09-899-471-1
; Sequence 1, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899, 471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (2218)
US-09-899-471-1

Alignment Scores: 0
Pred. No.: 3605.00
Score: 674
Percent Similarity: 100.0%
Length: 2256
Matches: 674
Conservative: 0

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Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Gaps: 0
Indels: 0
Mismatches: 0

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... 1-2-571) * 118-09-899-471-1 (1-2256)

[illegible]

RESULT 2
US-10-719-202-1
; Sequence 1, Application US/10719202
; Publication No. US20040121388A1

2

US-10-719-202-1

US-10-715-202 : sequence 1, Application US/10719202

Publication No. US20040121388A1

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; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (197) ... (2218)
US-10-719-202-1
Alignment Scores:
Pred. No.: 0 Length: 2256
Score: 3605.00 Matches: 674
Percent Similarity: 100.0% Conserved: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-719-202-2 (1-674) x US-10-719-202-1 (1-2256)
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DB 197 ATGCTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 257 CTGGAGAGACTGATGGAGCTCAGGACACGACGCTGCTCTAGGCTCTCTCTGCT 316
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 317 CTCTGGATGGTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 377 CTAGTGCCTACCGCTGACAGCGAGCTGTGCTGAGGTGTCCACAGAGACAGATTGC 436
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 437 GCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
DB 497 GAAGCTGGAAGTCTGATTGAGAACTCAGAGCTCAGAGCTTAGGAACGCTCTCTCCAGGCCAG 556
QY 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
DB 557 GTGGTGTCTCTCTTCCAGGCTTACCCCATCGCCGCTGTGCTGCTGCTGCTGCTGCTGCT 616
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 617 CCGCTGACCTGTGTGACGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
QY 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu 180
DB 677 GCTAGTCTTGGGGCTGAGGTACAGATCTGTGTCTTACACGAGGCCAGGTACCGAAGAG 736
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QY 201 GluGlnAspPheSerPheLeuLeuTrpLeuArgProValProAspAlaLeuLysSer 220
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QY 261 ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgVal 280
DB 977 CCTTCCGGGAGATCCCGTGCACACAGAACCTCTGSCACATAGCCAGGCTGCGGGTA 1036
QY 281 LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 300
DB 1037 CTGTCCCAAGGGTATGGCAGCTAGATGCGCTTGTGTCTGCGCGCAAGGTAACACTG 1096
QY 301 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnLys 320
DB 1097 TGCTGGCAGGCACACAGCAGAGTCCCTGCGCAGCTTGTGTGCCACAGTGCCCGCAAG 1156
QY 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
DB 1157 AACGCCACTGTGATGAGCCACAGATTTCCAGTTGCTGCGCAGCCACCCCAACTCTGT 1216
QY 341 ValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu 360
DB 1217 GTCCAGGTGAGCACCTGGGAGAGGTTGAGTGTCAAGCGTGTCTGCTGGGCTGACTCTCT 1276
QY 361 GlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeuAsnAnthrSer 380
DB 1277 GGGCCCTTCAAGGATGATATGCTGTGTAGTGGAGATGAAACCGGCTCTCAACACATCA 1336
QY 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
DB 1337 GTCTGTGCTTGGACCCAGTGTGTACCACTGCCAGCATGGCTTCCAGAGGCT 1396
QY 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
DB 1397 GCTGCGCTGGGAGAGGAGTGTGTGCAAGACTTCCGATCACACCAGTGTATGACGTGTGG 1456
QY 421 AsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrpIleHisArgArg 440
DB 1457 AACGATGACAAACATGGGATCGCTATGGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1516
QY 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
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QY 461 LeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
DB 1577 CTAAAAAAGGACCGCAGGAAAGCGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1636
QY 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
DB 1637 GCCGACGAGCGGCTTACGAGGCTGTGTGGAGACACTGCGCTGCGCTGCGCTGCGCTGCGCT 1696
QY 501 ProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeu 520
DB 1697 CCACTCGGCTGGCGCTGAGCTGTGGAGCGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1756
QY 521 AlaTrpPheHisGlnArgArgIleLeuGlnGluGlyValValIleLeuLeu 540
DB 1757 GCCTGGTTCCACACACGAGCGCGCTATCTTCCAGAGGGTGGCTGGTAACTCTCTCTC 1816
QY 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
DB 1817 TTCTCGCCCGCGCTGCGCAGTGTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1876
QY 561 GlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
DB 1877 GGGCCGATGACGCGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1936
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Tue Aug 22 11:34:35 2006

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1997 CCTCCCGGTTCCGGGTGCGCCGCTCTCTCTCCCTGCCCCACGACGCTGCGGGTTCCTG 2056
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621 AspAlaLeuGlnGlyCysSerThrSerThrSerThrSerThrSerThrSerThrSerThr 640
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2057 GATGCACTGCAGGAGGCTGCTCCACTTCGCGGGGCGACCCGCGGACCGGGTGGAAACGA 2116
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RESULT 3
US-09-899-471-4
; Sequence 4, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(2290)
US-09-899-471-4

Alignment Scores:
Pred. No.: 0 Length: 2328
Score: 3583.00 Matches: 674
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 0
Query Match: 99.4% Indels: 24
DB: 3 Gaps: 1

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Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 257 CTGGAGAGACTGATGGAGCCCTCAGACACTGCACGCTGCTCTTAGGCTCTCTCTGCCAC 316
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 317 CTCTGGGATGTGAGCTGCTCTGCTGCTGCTGGAGCCCTCCAGCTCTGCGCCCGGCGCTGTG 376
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 377 CTAGTGCCTACCGGCTCGACGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 436
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisThrAlaLeuProGlu 100
Db 437 GCCCTCCGGTCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 496
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 497 GAAGCTGGAAAGTCTGATTCAGAACTCCAGGAGTCTAGGAACGCGCTCTCTCCAGGCCCG 556

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Qy

141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db

617 CCGGCTGACCTGGTGAGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
Qy

161 AlaSerLeuGlyAlaGluValGlnLeuTrpSerTrpThrLysProArgTrpGlnLysGlu 180
Db

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Qy

181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db

737 CTCACCTCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
Qy

189 -----AspGlyAspAsnValLeuLeuThr 196
Db

797 AGCTGTGGGTCTCGCTCGCTCAATGTGTCTACAGATGGTGACAAATGTCTTCTTGACA 856
Qy

197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp 216
Db

857 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTGCTGCTGCTGCTGCTGCT 916
Qy

217 AlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnLeuThrLeuAsnHis 236
Db

917 GCTCTCAATCTCTGGTGTACAAAACCTGACTGGACCTCAGAAACATTAATTTAAACCCAC 976
Qy

237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
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977 ACAGACCTGGTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1036
Qy

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1037 GTCGAATTCGCCCCCTTCGCGGAGATCCCGGTGCACACAGGAACCTCTGCGCACATAGCC 1096
Qy

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Db

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Qy

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Qy

317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
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1337 GCTGACTCTCTGGGCGCTTCAAGGATGATATGTCTGTAGTGGAGATGAAAACCGGCGCTC 1396
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Db

1397 AACCAACATCAGTCTGTGCTTGGAACTGGAGCTGTACACCACTGCGCCAGCATGGCC 1456
Qy

397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
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Qy

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Db

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Qy

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1277 CCCAACCTCTGTCTCAGGTGAGCACCTCGGAGAGGTTTCAGCTGCAGCGTGTCTGTGG 1336
357 AlaAapSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
1337 GCTGACTCCTTGGGGCCCTTCAAGATGATATGCTTTAGTGGAGATGAACACCGGCTC 1396
377 AenAenThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
1397 AACACACATCAGTCTGTGCTTGGACCCAGTGGCTGTACACACATGCCCGCAGCATGCC 1456
397 SerThrArgAlaAlaArgLeuGlyGluGluLeuGlnAspPheArgSerHisGlnCys 416
1457 TCCACGAGAGCTGTCTCGCTGGGAGAGAGTGTCTGCAAGACTTCCGATCACACAGTGT 1516
417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
1517 ATGCAGCTGTGGAACATGACACATGGATCGCTATGGGCTGCCCATGGACAAAGTAC 1576
437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
1577 ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTACTCTTGGCTGCGCGCTTTTC 1636
457 PhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
1637 TTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1696
477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
1697 CTCCTCCACTCCGCGCAGCGAGCGGCTACGAGCGTCTGTGGAGCACTGGCGTCCGCG 1756
497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
1757 TTGAGCCAGATGCACATGGCGGTGGCGGTGGAGACCTGTGGAGCGCGCGAGCTGAGCGG 1816
517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgLysGluGlnGlyVal 536
1817 CAGGAGCCCTAGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1876
537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
1877 GTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1936
557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
1937 ACAGTGGAGCCCGGGCGCATGACGCCCTCGCCGCTTGGCTAGCTGCGTGTACTCCGAT 1996
577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
1997 TTCTTGCAGCGCGGGCGACCGGCGCTAGCTCGGGCTTACTTTCAGCGGCTGTGCAC 2056
597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
2057 CCAGACTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2116
617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
2117 CCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2176
637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
2177 CCGGTGGACAGATGACCCAGGCGCTGCGGTCCGCCCTCGGACAGCTGTACTTCTAGCTCG 2236
657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
2237 GAAGCCCGAGCTGTCTGAGGAATGGAGCCTGGGACCCCTGCACACTACTAGAA 2290

RESULT 5
US-11-150-533-25

Sequence 25, Application US/11150533
Publication No. US20060002925A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Burkhead, Steven K.
APPLICANT: Levin, Steven D.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
APPLICANT: Jaspers, Stephen R.
APPLICANT: Billsborough, Janine
TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 04-06P1
CURRENT APPLICATION NUMBER: US/11/150,533
CURRENT FILING DATE: 2005-06-10
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 2269
TYPE: DNA
ORGANISM: Mus musculus
US-11-150-533-25
Alignment Scores:
Pred. No.: 0 Length: 2269
Score: 3572.50 Matches: 671
Percent Similarity: 98.4% Conservative: 1
Best Local Similarity: 98.2% Mismatches: 2
Query Match: 99.1% Indels: 9
Gaps: 1
DB: 1
US-10-719-202-2 (1-674) x US-11-150-533-25 (1-2369)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 197 ATGCTGTGTCTCTGTCT 256
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 257 CTGAGAGACTGTATGGAGCCCTCAGGACACTGACGCTCTCTCTCTCTCTCTCTCTCTCTCT 316
Qy 41 LeuTrpAspGlyAspValLeuLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 317 CTCGTGGATGTGTGACGTCT 376
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 377 CTAGTGCCTACCGGCTGCAGACGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 436
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 437 GCCCTCTGTGTCCTGT 496
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnSerArgAsnAlaSerLeuGlnAlaGln 120
Db 497 GAAGCTGGAAGTCTCATTCAGAACTCCAGGAGTCTAGGAGCGCTCTCTCTCTCTCTCTCTCT 556
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 557 GTGGTGTCTCTCTCTCAGGCTTACCCCATCGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 616
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 617 CCGCTGACCTGTGTGAGCGCTGT 676
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 677 GCTAGTCTTTGGGCTGAGGTACAGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 736
Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAsp 191
Db 737 CTCACACTCACACAGCAGCTGTCT 796

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QY 192 AsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeu 211
DB 797 AATGTCCTCTGACACTGGATGCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTG 856
QY 212 ArgProValProAspAlaLeuLysSerLeuTyrTrpLysAsnLeuThrGlyProGlnAsn 231
DB 857 CGTCCAGTCCCGATGCTCTCAATCCCTTGTGGTACAAAACCTGACTGAGCCTCAGAAC 916
QY 232 IleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGlu 251
DB 917 ATTACTTTAAACACACAGACCTGGTTCCCTGCTCTGCAATTGAGGTGTGGTGCCTAGAG 976
QY 252 ProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 271
DB 977 CCAGACTCTGAGAGGGTCAATTCCTGCCCTTCGGGAAGATCCCGTGACACAGGAAC 1036
QY 272 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaPro 291
DB 1037 CTCTGGCACATAGCCAGGCTGCGGGTACTGTGCCCAAGGGTATGGCAGCTAGATGCGCCT 1096
QY 292 CysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGln 311
DB 1097 TGTCTGCTCCGGGCAAGGTAACTGTCTGGAGGACACACAGCAGAGTCCCTGCCAG 1156
QY 312 ProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGln 331
DB 1157 CCACCTGTGCCACAGTGGCCCCAGAGAACGCCACTGTGAATGAGCCACAGATTTCCAG 1216
QY 332 LeuValAlaGlyHisProLeuLeuCysValGlnValSerThrTrpGluLysValGlnLeu 351
DB 1217 TTGGTGGCAGGCCACCCCACTCTGTCTGAGGTGAGCACCCTGGGAGAGGTTTACGTG 1276
QY 352 GlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGlu 371
DB 1277 CAAGCGTGTGTGGGGTGACTCCTTGGGGGCCCTTCAAGGATGATGTGTTAGTGGAG 1336
QY 372 MetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrPro 391
DB 1337 ATGAAAACCGGCTCAACACACATCAGTCTGTGGCTTGGNACCCAGTGGCTGTACACCA 1396
QY 392 LeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPhe 411
DB 1397 CTGCCACAGATGGCTCCACAGAGCTGTCTGCTGGAGAGGTTGCTGCAAGACTTC 1456
QY 412 ArgSerHisGlnCysMetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCys 431
DB 1457 CGATCACACAGTGTATGACAGCTGTGGNACGATGACACATGGGATCGCTATGGGCTGC 1516
QY 432 ProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeu 451
DB 1517 CCATGTGACAGTACATCCACAGCGCTGGTCTGTAGTATGGCTGGCTGGCTTCTTGTG 1576
QY 452 AlaAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGly 471
DB 1577 GCTGCGCGCTTTTCTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1636
QY 472 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGly 491
DB 1637 TCCCGACAGCGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1696
QY 492 AlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArg 511
DB 1697 GCATGTGGGTCCCGTTGACAGATGCCACTGCGGTGGCCGTGGACCTGTGGAGCCGC 1756
QY 512 ArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgGlyLeu 531
DB 1757 CGCGAGCTGAGCGCGCAGCGAGCCCTAGCTGTGTCTCCACCCAGCAGCGCGGTATCCTG 1816
QY 532 GlnGluGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGln 551
DB 1817 CAGGAGGGTGGGTGTAATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1876
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QY 552 TrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSer 571
DB 1877 TGGCTCAGCTCCAGACAGTGGAGCCGCGCGCATGAGCCCTCGCGCGCTGGCTCAGC 1936
QY 572 CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPhe 591
DB 1937 TGGCTGCTACCCGATTTCTGCAAGGCCGCGCGCATGAGCCCTCGCGCGCTGGCTCAGC 1996
QY 592 AspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSer 611
DB 1997 GACGGGCTGCTGCACCCAGACTCTGTGCCCTCCCGCTCGCGCTGGCGCTCTTCTCC 2056
QY 612 LeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla 631
DB 2057 CTGCCCTCGCAGCTGCGGCTTCTTCTGATGCACTGACAGGAGGCTGCTCCTCCTCCGCG 2116
QY 632 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSer 651
DB 2117 GGGCGACCCGCGAGCCGCGTGGAAACGAGTGACCCAGGCGCTGGCGCTCGCGCTGGAC 2176
QY 652 CysThrSerSerSerGluAlaProGlyCysGluGluTrpAspLeuGlyProCysThr 671
DB 2177 TGTACTTCTAGCTCGGAGCCCGAGGCTGCTGCGAGGATGGGACCTGGGACCTGGACT 2236
QY 672 ThrLeuGlu 674
DB 2237 ACACTAGAA 2245
RESULT 6
US-11-150-533-29
; Sequence 29, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-150-533-29
Alignment Scores:
Pred. No.: 0 Length: 2287
Score: 3569.50 Matches: 671
Percent Similarity: 97.5% Conservatives: 1
Best Local Similarity: 97.4% Mismatches: 2
Query Match: 99.0% Indels: 15
DB: 16 Gaps: 1
US-10-719-202-2 (1-674) x US-11-150-533-29 (1-2287)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
DB 197 ATGCGCTGTCTCTGGTTCTCTGCTGTCTTGGCAGCTGGGCGGAAACCTGTGGTGGTCTCT 256
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 257 CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTGCTCTTAGGCGCTCTCTGCCAC 316
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
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;
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; OTHER INFORMATION:
; NAME/KEY: mat peptide
; LOCATION: (259)..()
; OTHER INFORMATION:
US-09-863-818A-7

Alignment Scores:
Pred. No.: 0 Length: 2314
Score: 3565.00 Matches: 671
Percent Similarity: 96.3% Conservative: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 3 Gaps: 1

US-10-719-202-2 (1-674) x US-09-863-818A-7 (1-2314)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
DB 199 ATGCCCTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 259 CTGGAGAGACTGATGAGGCTCTAGGACATGACAGCTGCTCTCTAGGCTCTCTGCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 319 CTCTGGAGTGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 379 CTAGTGCCTACCGGCTGACAGCGAGCTGGTGTCTGAGGTGTCCACAGAGACAGATTGC 438
QY 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 439 GCCCTCTGTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
DB 499 GAAGCTGGAAGTCTGATTCAGAACTCCAGGACTCTAGGAACGCTCTCTCCAGGCCAG 558
QY 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
DB 559 GTGGTGTCTCTCTCCAGGCTACCCCATCGCCGCTGTGCTGCTGCTGCTGCTGCTGCTG 618
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 619 CCGCTGTACTGTGTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678
QY 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
DB 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGTCTCTACAGNAGCCAGGTACCAAGAGAG 738
QY 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
DB 739 CTCAACCTCACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
QY 189 -----AspGlyAspAsnValLeuLeuThr 196
DB 799 AGCTGTGGGTCTGCCCTTGGCTCAATGTGTCTACAGATGTGTGACAAATGTCTTGTGCA 858
QY 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
DB 859 CTGGATGTCTCTGAGAGAGAGGACTTGTAGTCTTCTTACTGTACTGTGTGTGTGTGTGT 918
QY 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
DB 919 GCTCTCAAAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 978
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QY 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
DB 979 ACAGACCTGTGTTCCCTGCTCTGCAATTCAGGTGTGTGCTAGAGCCAGACTCTGTGAGG 1038
QY 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
DB 1039 GTCGAATTCCTGCCCTTCCGGGAAGATCCGGGTGCAACACAGGAACTCTGTGGCACA 1098
QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
DB 1099 AGGCTCGGGTACTGTCCCGAGGGTATGACAGTAGATGCGCTTGTGTCTGTCCGCGGC 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
DB 1159 AAGGTAACACTGTGCTGGCAGGCACACAGAGTCCCTGTCAGCCACTGTGTGCCACCA 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
DB 1219 GTGCCCCAGAGAACGCCACTGTGTAATGAGCACAAAGATTTCAGTTGTGTGGCAGGCC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLeuValGlnLeuGlnAlaCysSerTrp 356
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QY 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
DB 1339 GCTGACTCTCTGGGGCCCTTCAAGGATGATATGCTGTGTAGTGAGATGAATAACCGG 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
DB 1399 AACCAACATCATGCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluLeuGlnAspPheArgSerHisGlnCys 416
DB 1459 TCCACAGAGCTGCTGCTGCGCTGGAGAGGAGTGTCTGCAAGACTTCCGATCACACAGTGT 1518
QY 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
DB 1519 ATGCAGCTGTGNAACGATGACACATGGATCGCTATGGCCCTGCCCATGGACAGTAC 1578
QY 437 IleHisArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
DB 1579 ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTACTCTTGTGCTGCGGCTTTTC 1638
QY 457 PhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
DB 1639 TTCTTCTCTCTTCTAAAAAAGGACCGCAGGAAAGCGCGCTGCTGCCGACGCGCTTG 1698
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
DB 1699 CTCCTCCACTCTCGCCAGCGAGCGGGCTACGAGCGCTGCTGGAGACACTGGGCTCGCG 1758
QY 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
DB 1759 TTGAGCCAGATGCCACTGCGCTGGCGGTGGACCTGTGTGGAGCCGCGCGAGCTGAGCG 1818
QY 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
DB 1819 CACGAGCGCTAGCTGTGTTCACCAACCGACCGCGCTATCTCTGTCAGGAGGGTGGCGTG 1878
QY 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnTrpLeuGlnLeuGln 556
DB 1879 GTAATCTTCTCTCTCGCCCGCGCGGTGGCGCGAGTGTGACAGTGGCTGTGAGCTCCAG 1938
QY 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
DB 1939 ACAGTGGAGCCCGGGCCGATGACGCCCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1998
QY 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
DB 1999 TTCTCTCAAGGCGCGCGACCGCGCTACGTCGGGCTACTTTCAGCGGCTGTGTCAC 2058
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QY 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTGTGTCCTCCCGTTCGCGTTCGCGCGCTCTTCTCCCTCCCTCGCAGCTG 2118
QY 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTCTCGATGCACTGCAGGAGGCTGCTCATTCCGCGGGCGACCCGCGAC 2178
QY 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACAGTGCACCGCGCTGCGTCCGCGCTGGACAGCTGTACTTCTAGCTCG 2238
QY 657 GluAlaProGlyCysGlyGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGCTGGAGGAATGGGACCTGGGACCTGCACTACACTAGAA 2292

RESULT 8
US-10-749-144-7
; Sequence 7, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (259)..()
US-10-749-144-7

Alignment Scores:
Pred. No.: 0 Length: 2314
Score: 3565.00 Matches: 671
Percent Similarity: 96.3% Conservatives: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 9 Gaps: 1

US-10-719-202-2 (1-674) x US-10-749-144-7 (1-2314)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 199 ATGCCTGTGCTCTGTTCTCTGCTGCTTGGCACCTGGCGCGAAACCTGTGTCGTCTCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGAGGCTCAGGACATGCACGCTGCTCTCTAGGCTCTCTCTGCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCTGGATGGTGACGTGCTCTGCTGCTGCTGGAAGCTCCAGTCTGCCCGCAGGCCCTGTG 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 379 CTAGTGCCTACCGGCTGCAGACGAGCTGCTGAGGTGTCCACAGAACAGATTGC 438
QY 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCCTCTGTGCTGTGGTGGTCCACTTGGCCGTGATGGGACCTGGGCGAGGCTGAA 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
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Db 499 GAAGCTGGAAAGTCTGATTCCAGAACTCCAGAGCTAGGAACGCTCTCTCCAGGCCAG 558
QY 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
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QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 619 CCCGCTGACCTGGTGGAGCTGGTTCAGTCCGCTGGGTCTCGCGTATTGTGACTGTTCCAG 678
QY 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 679 GCTAGTCTTGGSGCTGAGGTACAGATCTGTGCTTACACGAAGCCAGGTACAGAAAGAG 738
QY 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 739 CTCAACCTCACACAGCAGCTGCCCTGACTGCGAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
QY 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 799 AGCTGCTGGGTCTCGCCCTGGCTCAATGTGTCTACAGATGCTGACAATGTCTTCTGACA 858
QY 197 LeuAspValSerGluGlnGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTCTGCTGCTCCAGTCCGGAT 918
QY 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 919 GCTCTCAATCTTTGTGGTCAAAAACCTGACTGACCTCAGAACATTACTTTAAACAC 978
QY 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
Db 979 ACAGACCTGGTTCCTTGCTCTGCACTTCAGTGTGCTGCTAGAGCCAGACTCTCAGAGG 1038
QY 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 1039 GTCGAATCTGCCCCCTTCGGGAGAGATCCCGGTGCACACAGAACTCTCGGCACATAGCC 1098
QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
Db 1099 AGGCTGCGGGTACTGTCCCCAGGGGTATGGACGTAGATGGCTTGTGTGTCTGCGGGC 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTAACACTGTGCTGGCAGGCACACAGACAGAGTCCCTGCGAGCCACTTGTGCCACCA 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAAAGACCGCACTGTGAATGAGCCACCAAGATTTCAGTTGTTGGCAGGCCAC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1279 CCCAACCTCTGTGTCCAGGTGAGCACTGGGAGAAGGTTCACTGCAAGCGTGTGTGTGG 1338
QY 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAACCCGCGCTC 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACCAACACATCATGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCACAGAGAGCTGCTCGCTGGAGAGGAGTTGCTGCTCAAGACTTCGATCACACAGTGT 1518
QY 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
Db 1519 ATGCAGCTGTGGAACGATGACAACTGGGATCGCTATGGGCTGCCCCATGCAAGATAC 1578
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Qy LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db CTCTTCACTCTCCGCGAGCGGCTAGCAGCGCTTGGTGGGAGCACTGGCGTCCGCG 1758
Qy LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla 516
Db TTGAGCCAGATGCCACTGCGCGTGGCGTGGCTGACCTGGAGCGCCCGGAGCTGAGCGCG 1818
Qy HisGlyAlaLeuAlaTrpPheHisGlnArgArgGlnLeuGlnGluGlyVal 536
Db CACGAGCGCTAGCTGGTTCACACACAGCGCGCTATCTCTGAGAGGGTGGCGTG 1878
Qy ValLeuLeuLeuPheSerProAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db GTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1879
Qy ThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAsp 576
Db ACAGTGGAGCCCGCGCGCGCAGCGCTCTCGCGCTGGCTGAGCTGCTGCTACCGGAT 1998
Qy PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db TTCTTCAAGCGCGCGCGCGCTAGCTGGGGTCTACTTCCGAGCGGGTGGTGCAC 2058
Qy ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db CCAGACTCTGTGCGCTCTCCGCGTTCGCGTGGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 2059
Qy ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db CCGGCTTTCTTGTGATGCATGCGAGGGAGGCTGCTCCACTTCCGCGGGCGCACCGCGGAC 2178
Qy ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db CCGGTGGAGCGAGTGACCGAGCGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 2179
Qy GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrThrLeuGlu 674
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RESULT 9

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US-10-924-667-7
; Sequence 7, Application US/10924667
; Publication No. US2005009145A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: DX01170K
; CURRENT FILING DATE: 2004-08-23
; PRIOR FILING DATE: 2004-08-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide

; LOCATION: (259)..( )
; OTHER INFORMATION:
; US-10-924-667-7

Alignment Scores: 0 Length: 2314
Pred. No.: 3565.00 Matches: 671
Score: 96.3% Conservative: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 9 Gaps: 1

US-10-719-202-2 (1-674) x US-10-924-667-7 (1-2314)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 199 ATGCTGTGTCTCTGTGTCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 258
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGGAGCGCTCAGGACACTGACGCTGCTCTCTAGGCTCTCTCTGCTGCT 318
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCTGGATGTGTGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 379 CTAGTGTCTTACCGCTCTGACGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
Qy 101 GluAlaGlySerSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 499 GAAGCTGGAAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAAACGCTCTCTCTCCAGG 558
Qy 121 ValValLeuSerPheGlnAlaTyrProLeuAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 559 GTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 619 CCGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678
Qy 161 AlaSerLeuGlyAlaGluValGlnTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTCTACAGAAAGCCAGGTACAGAAAGAG 738
Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAspAsnValLeuLeuThr 188
Db 739 CTCAACTCACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 799 AGCTGCTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 858
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTCTGTACCTGCTGCTGCTGCTGCTG 918
Qy 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnLeuThrLeuAsnHis 236
Db 919 GCTCTCAAAATCTTGTGGTACAAAAACCTGACCTGGACCTCAGAACATTACTTTAAACCC 978
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
Db 979 ACAGACTGTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 1039 GTCGAATTTCTGCGCTTCCGGGAAGATCCGGTGCACACAGGAACCTCTGCGCACATAGCC 1098
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QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
Db 1099 AGGCTGCGGGTACTGTCTCCCAAGGGGTATGGCAGCTAGATGGCCCTTGTCTGTGCGGGC 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTAAACACTGTGTGGCAGCCACAGACCAGAGTCCCTGCCAGCCACTTGTGCCACCA 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAAAGACGCCACTGTGAATGAGCACAAGATTTCAGTTGGTGGCAGGCCAC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1279 CCCAACCTCTGTGTCCAGTGTGACACTGGGGAAGGTTTCAGCTGCAAGCGTGTGTGG 1338
QY 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAACCGGCCCTC 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACAAACATCAGTCTGTGCTTGGNACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCCACGAGAGCTGCTCGCTGGGAGAGGAGTGTCTGCAAGACTTCGGATCACACCAAGTGT 1518
QY 417 MetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrp 436
Db 1519 ATGCAGCTGTGGAAACGATGACAACTGGATGGCTATGGGCTGCCCTCATGGACAAAGTAC 1578
QY 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1579 ATCCACAGCGCTGGGTCTAGTATGGCTGGCTTCGCTACTCTTGGCTGGCGGCTTTTC 1638
QY 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1639 TTCTTCTCTCTTCTAAAGAGACCGCAGAAAGCGGCCGCTGGCTCCCGCAGCGCCCTTG 1698
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1699 CTCCTCCATCTCGCCGACGAGCGGCTACGAGCGCTGGTGGAGCACTGGCGTCCGGC 1758
QY 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
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QY 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
Db 1819 CACGGAGCCCTAGCCTGGTTCCACCAACGACGACGCGGTATCTCGAGGAGGTGGCGTG 1878
QY 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1879 GTAATCTTCTCTTCTGCGCCGCGCGCTGGCGCAGTGTGACGAGTGGCTGCCAGTCCAG 1938
QY 557 ThrValGlnProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
Db 1939 ACAGTGGAGCCGCGCGCATGACGCCCTCGCGCCCTGGCTCAGCTGCGGTGTACCCGAT 1998
QY 577 PheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTrpPheAspGlyLeuLeuHis 596
Db 1999 TTCCTGCAAGCGCGGGGACCGGCCGCTACTGCGGGTCTACTTCGAGCGGCTGTGTCAC 2058
QY 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCCCTCCCCGTTCCGGCTGCGCGCTCTCTCTCCCTGCGCCCTCGCAGCTG 2118
QY 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTTCCTGGATGACTGCAGGGAGGCTGTCTCCACTTCCCGCGGGGCGACCCCGCGGAC 2178

QY 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACGAGTGACCCAGGCGCTGCCGTCCCTCGACAGCTGTACTTCTAGCTCG 2238
QY 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGCTGCGGGAATGGACCTGGGACCTCGCACTACACTAGAA 2292
RESULT 10
US-09-866-050A-487
; Sequence 487, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.101IC4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-487
Alignment Scores:
Pred. No.: 0 Length: 2128
Score: 3562.00 Matches: 670
Percent Similarity: 96.3% Conservative: 2
Best Local Similarity: 96.0% Mismatches: 24
Query Match: 98.8% Indels: 24
DB: 3 Gaps: 1
US-10-719-202-2 (1-674) x US-09-866-050A-487 (1-2128)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 1 ATGCCTGTGTCTGCTTCTCTGTCTTGGCACTGGGCGGAAACCCCTGTGGTCTCTCT 60
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 CTGGAGAGACTGATGGAGCCTCAGGACACTGACAGCTGCTCTCTAGGCTCTCTCTGCCAC 120
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 CTCTGGATGGTGACGTGCTCTGCTGCTGGAGCCTCCAGTCTGCCCGGCGGCTGTG 180
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 CTAGTGCCTTACCCGCTCGACAGCGAGCTGGTGGCTGAGGTGTCACAGAGACAGATTGC 240
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisIleTrpAlaGluProGlu 100
Db 241 GCCCTCTGTGTCCTGTGGTGTCCACTTGGCCGTGCATGGGCATCTGGGCGAGGCTGAA 300
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTTAGGAACGCTCTCTCCAGGCCAG 360
QY 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 361 GTGGTGTCTCTCTTTCAGGCTTACCCCATCGCCCGCTGTGGCTGTGCTGTGAGGTCCAGGTG 420
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCGGCTGACTGGTGGAGCTGTGCTCAGTCCGTGGGTCTTCCGGTATTTGACTGTTCGAG 480

Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCTAGTCTGGGGCTGAGGTACAGATCTGGTCTTACACAGAGCCAGGTACAGAGAG 540
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 541 CTCACCTCACACAGCAGCTGCCTGACTGCGAGGGTCTTGAAGTCCGGGACGATCCAG 600
Qy 189 -----AspGlyAspAsnValLeuThr 196
Db 601 AGCTGCTGGGTCTGCCCTGGCTCAATGTGTCTACAGATGGTGACATGTCCTTCTGACA 660
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
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Qy 217 AlaLeuLysSerLeuTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 721 GCTCTCAAAATCTTGTGGTACAAAACCTGACTGGACCTCAGAACATTACTTTAAACAC 780
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
Db 781 ACAGACCTGGTTCCTCCCTCTGCAATTCAGGTGGTGGCTAGAGCCAGACTCTCTGAGAG 840
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 841 GTCGAATCTGCCCTTCCGGAGAGATCCCGGTGCACACAGGAACCTCTGGCACATAGCC 900
Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
Db 901 AGGTGCGGGTACTGTCCCGAGGGGTATGGCAGCTAGATGCGCTTGTCTGTCTGCCGGC 960
Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 961 AAGTAACTGTCTGGCAGGCCACAGACAGAGTCCCTGCCACGCCACTTGTGCCACCA 1020
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1021 GTGCCCCAGAGAAGCCACTGTGAATGAGCCACAGATTTCCAGTTGGTGGCAGGCCAC 1080
Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1081 CCCAACTCTGTGTCCAGGTGAGCACCCTGGGAGAGGTTTCAGCTGCAAGGTGCTGTGG 1140
Qy 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
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Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1201 AACACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGATGGCC 1260
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1261 TCCACGAGAGCTGCTGCCCTGGGAGAGGTTGCTGCAAGACTTCCGATCACACCAAGTGT 1320
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Db 1381 ATCCACAGGCGCTGGGTCTAGTATGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTTTC 1440
Qy 457 PhePheLeuLeuLeuLysLysAspArgArgLysAlaAlaAlaArgGlySerArgThrAlaLeu 476
Db 1441 TTCTTCTCTCTTAAAAAAGGACCGCAGGAAGCGGCCCTGGCTCCCGCACGGCCCTTG 1500
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1501 CTCTCTCACTCCGCGCAGCGAGGGGTACAGCGTCTGTGGAGCACTGGGCTCGCG 1560

Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla 516
Db 1561 TTGAGCCAGATGCACCTGGCGTGGCGGTGGACCTGTGGAGCGCGCGAGCTGAGCGCG 1620
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
Db 1621 CACGGAGCCCTAGCCTGGTTCCACCCAGCAGCGCGGTATCTTGCAGGAGGGTGGCGTG 1680
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1681 GTAATCTTCTTCTTCCCGCGCGCGGTGGCGCAGTGTTCAGCAGTGGCTGCAGCTCCAG 1740
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
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Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTCTTCAAGGCCCGGCGGACCCGCCCTAGTCCGGGTCTTCTTGCACGGGCTGTGCAC 1860
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCAGACTCTGTGCCCTCCCGTTCGCGTTCGCGTCCCGCTCTTCTCCCTGCGCTGCAGCTG 1920
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCGGCTTCTCGATGCATGCAGGAGGCTGTCCACTTCCGCGGGCGACCCGCGGAC 1980
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 1981 CGGGTGGAAACGAGTGACCCAGGCGCTGCGGTCCGCGCTGAGCAGCTGTACTTCTACCTCG 2040
Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GAAGCCCCAGGCTGCTCGAGGAGATGGGACCTGGGACCTGCATACACTAGAA 2094

RESULT 11

US-10-152-661-487
; Sequence 487, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011C5
; CURRENT APPLICATION NUMBER: US/10/152,661
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-487

Alignment Scores:				
Pred. No.:	0	Length:	2128	
Score:	3562.00	Matches:	670	
Percent Similarity:	96.3%	Conservative:	2	
Best Local Similarity:	96.0%	Mismatches:	24	
Query Match:	98.8%	Indels:	1	
DB:	6	Gaps:		

US-10-719-202-2 (1-674) x US-10-152-661-487 (1-2128)

Qy	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer	20
Db	1	ATGCCTGTGTCCTGGTTCCTGCTTCCTTGGCACTGGGCCGAAACCTGTGGTCTCTCT	60
Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGACCGTCTCTCTAGGCCTCTCTGCGCAC	120
Qy	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	121	CTCTGGGATGTGACGTCTCTGCCTGCTCGAAGCCTCCAGTCTGCCCCAGGCCCTGTG	180
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
Db	181	CTAGTGCCCTACCGCGCTCGACAGGAGCTGGTGTCTAGTGTCTCCAGAAACAGATTGC	240
Qy	81	AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
Db	241	GCCCTCTGTGTCGCGTGTGGTGTCCACTGGCCGTGCATGGGCACTGGGCGAGCGCTGAA	300
Qy	101	GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln	120
Db	301	GAACTGGAAATCTGATTCAAGACTCCAGGAGTCTAGGAAGCCCTCTCTCCAGGCCACG	360
Qy	121	ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal	140
Db	361	GTGGTGTCTCTCTCCAGGCCCTACCCATCGCCCGCTGTGCCCTCTGTGAGGTCCAGGTG	420
Qy	141	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
Db	421	CCCGCTGACCTGGTGGCAGCCTGGTCAGTCCGCGGGTTCTGCGGTATTGACTGTTCGAG	480
Qy	161	AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu	180
Db	481	GCTAGTCTTGGGGCTCAGGTACAGATCTGCTCTACACGAAGCCAGGTACCAGAAAGAG	540
Qy	181	LeuAsnLeuThrGlnGlnLeuPro-----	188
Db	541	CTCAACCTCACACAGCAGCTGCCCTGACTCGAGGGGTCTTGAAGTCCGGGACAGCATCCAG	600
Qy	189	-----AspGlyAspAsnValLeuLeuThr	196
Db	601	AGCTGTGGTCTCTGCCCTGGCTCAATGTGTCTACAGATGGTGACAATGTCTCTTGTGACA	660
Qy	197	LeuAspValSerGluGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp	216
Db	661	CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTTACTGTACTGGTCCAGTCCCGGAT	720
Qy	217	AlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis	236
Db	721	GCTCTCAATCCCTTGTGGTACAAAAACCTGACTGGACCTCAGAACAATTACTTTTAAACCAC	780
Qy	237	ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg	256
Db	781	ACAGACTGTGTCCCTGCCCTCTGCATTTCAGTGTGGTGTGGCTAGAGCCAGACTCTTGAGAGG	840
Qy	257	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla	276
Db	841	GTCGAATCTTGCCCTTCCGGGAAGATCCCGGTGCAACACAGGAACCTCTGCGCATAGCC	900
Qy	277	ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly	296

901	Db	AGGCTCGGGTACTGTCCCAGGGGTATGGCAGCTAGATGCGCCTTGCTGTCTCTCCCGGGC	960
297	Qy	LysValThrLeuCysTrpGlnAlaProaspGlnSerProCysGlnProLeuValProPro	316
961	Db	AAGGTAACACTGTGCTGGCAGGCACACAGCAGAGTCCTCTGCCAGCACTTGTGCCACCA	1020
317	Qy	ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis	336
1021	Db	GTCCCCCAGAAGAACGCCACTGTGAATGAGCCACAAGATTTCCAGTTGGTGCCAGGCCAC	1080
337	Qy	ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp	356
1081	Db	CCCAACCTCTGTCTCAGGTGACCACTCGGGAGAAAGTTCAAGTCGCAAGCGTGTGTGG	1140
357	Qy	AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu	376
1141	Db	GCTGACTCCTTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAATAACCGGCCTC	1200
377	Qy	AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla	396
1201	Db	AACACACATCACTCTGTGCTTGGAAACCACTGGGTGTATACACCACTGCCCAGCATGGCC	1260
397	Qy	SerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCys	416
1261	Db	TCCACGAGAGCTGCTCGCTTGGAGAGGAGTTGCTGCAAGACTTTCGATTCACACCACTGT	1320
417	Qy	MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr	436
1321	Db	ATGCAGCTGTGGAAACGATGACACATGGGATCGCTATGGCTCGCCCATGTGACAAAGTAC	1380
437	Qy	IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe	456
1381	Db	ATCCACAGGCGCTGGGTCTTAGTATGGCTGGCTGCTCTACTCTTGCTCGGGCGCTTTTC	1440
457	Qy	PhePheLeuLeuLeuLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu	476
1441	Db	TTCTTCCTCTCTTAAATAAAGACCGCAGAAAGCGCCGTGGCTCCGCACGGCCTTG	1500
477	Qy	LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla	496
1501	Db	CTCCTCCACTCCGCGCAGGAGCGGCTACGAGCGTCTGTGTGGAGCATCTGGCGTCCGCG	1560
497	Qy	LeuSerGlnMetProLeuArgValAlaValaLaspLeuTrpSerArgArgGluLeuSerAla	516
1561	Db	TTGAGCCAGATGCCACTCGCGGTGGCCGTGGACCTGTGGAGCCGCCGCGAGCTGACGCG	1620
517	Qy	HisGlyAlaLeuAlaTrpPheHisGlnArgArgIleLeuGlnGlyGlyVal	536
1621	Db	CACGGAGCCCTAGCTGGTTCCACACACGACGACGCGGTATCTTCGAGGAGGTGGCGTG	1680
537	Qy	ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln	556
1681	Db	GTAATCCTTCTCTCTCGCCCGCGCGCGTGGCGAGTGTACGAGTGGCTGCAGCTCCAG	1740
557	Qy	ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp	576
1741	Db	ACAGTGGAGCCCGGCGCATGACGCCCTCGCCCGCTGGCTCAGTTCGCTGTACCCGAT	1800
577	Qy	PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis	596
1801	Db	TTCTTGCAAGGCGGGCGACCGCGCGTACGTCGGGGTCTACTTCGACGGGTGCTGCAC	1860
597	Qy	ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu	616
1861	Db	CCAGACTCTGTGCCCTTCCCGGTTCCGCGTCGCCCGCTCTTCTCCCTGCCCTCGACGCTG	1920
617	Qy	ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp	636
1921	Db	CCGGCTTTCTTGATGCACTGCAGGAGGAGCTGCTCACTTCGCGGGGCGACCCCGCGAC	1980
637	Qy	ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer	656
1981	Db	CGGGTGGAACTGAGTGAACCAAGCGGTGGGTCCGCGCTTGGACAGCTGTACTTCTACCTCG	2040

Qy 657 GluAlaProGlyCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
 Db 2041 GAAGCCCCAGGCTGCTGGAGGATGGACCTGGGACCCCTGCACCTACTAGAA 2094

RESULT 12
 US-10-416-442A-74
 ; Sequence 74, Application US/10416442A
 ; Publication No. US20040171109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haudenschild, Dominik
 ; APPLICANT: Rose, Larry
 ; APPLICANT: Moseley, Timothy
 ; APPLICANT: Reddi, A. Hari
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: IL-17 Receptor-Like Protein, Uses Thereof, and
 ; TITLE OF INVENTION: Modulation of Catabolic Activity of IL-17 Cytokines on
 ; TITLE OF INVENTION: Bone and Cartilage
 ; FILE REFERENCE: 023070-115511US
 ; CURRENT APPLICATION NUMBER: US/10/416,442A
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 74
 ; LENGTH: 2331
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: mouse IL-17RL cDNA with untranslated regions
 US-10-416-442A-74

Alignment Scores:
 Pred. No.: 0 Length: 2331
 Score: 3539.00 Matches: 666
 Percent Similarity: 95.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 7
 Query Match: 98.2% Indels: 24
 DB: 8 Gaps: 1

US-10-719-202-2 (1-674) x US-10-416-442A-74 (1-2331)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
 Db 199 ATGCTGTGTCTCTGGTTCCTGTCTGCTTGGCACTGGGCGGAAACCCCTGTGGTCTCT 258

Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 259 CTGGAGAGACTGATGGAGCTCAGGACACTGACGCTGCTCTTAGGCTCTCTCTAGCCCTCTCTG 318

Qy 41 LeuTrpAspGlyaspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 319 CTCTGGGATGGTACGCTCTGCTGCTGCTGGAAGCTCTCAGTCTGCCCCAGGCCCTGTG 378

Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 379 CTATGTGCTACCCGCTGACAGAGAGCTGGTCTGAGGGTCTCAGAGAGACAGATTGC 438

Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 Db 439 GCCTCTGTCTCGTGTGGTGTCCACTTGGCCGTGCTAGGCACTGGGCAGAGCCCTGAA 498

Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
 Db 499 GAAGCTGGAAGTCTGATTGAGAACTCCAGAGTCTAGGAACGCTCTCTCCAGGCCAG 558

Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
 Db 559 GTGGTGTCTCTCTCCAGGCTTACCCCATGCCCGCTGTGCCCTGTCTGGAGGTCCAGGTG 618

Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 Db 619 CCCGCTGACCTGGTGCAGCTGGTCCGTCCGTGGTCTCTCGGGTATTTGATGTGTTCCGAG 678

Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
 Db 679 GCTAGTCTTGGGCTGAGGTACAGATCTGTCTTACACGAAGCCAGGTACCAAGAAAGAG 738

Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
 Db 739 CTCAACCTCACACAGCAGCTGCTGACTGTCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798

Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
 Db 799 AGCTGCTGGGTCTGCCCTCGCTCAATGTGCTTACAGATGCTGACAATGTCTCTTGACA 858

Qy 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
 Db 859 CTGGATGTCTCTGAGGACAGGACTTTAGCTTCTTACTGTACCTGCTGCTGCTGCTGCTGCTG 918

Qy 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
 Db 919 GCTCTCAATCTTGTGGTACAAAACCTGACTGGACCTCAGAACATTACTTTAAACCAC 978

Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
 Db 979 ACAGACTGTGTTCCCTGCTCTGCAITTCAGTGTGGTCTGCTAGAGCCAGACTCTCTGAGAG 1038

Qy 257 ValGluPheCysProPheArgGluAspProGlyValaHisArgAsnLeuTrpHisIleAla 276
 Db 1039 GTCGAATTCGCCCCCTTCGGGGGAAGATCCCGGTGCACACAGGAACCTCTGGCATAGCC 1098

Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
 Db 1099 AGGCTGGGGTACTGTCCCCAGGGGTATGGCAGCTAGATGGCTGTCTGTCTGCCGGGC 1158

Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
 Db 1159 AAGGTAACTGTGTCTGGCAGGCACCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218

Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
 Db 1219 GTGCCCCAGAGAAGAACGCCACTGTGAATGAGCCACAAGATTTCCAGTTGGTGGGAGGCCAC 1278

Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
 Db 1279 CCCNACTCTGTGTCTCAGGTGAGCCTGGGAGAGGTTTCCAGCTGCAAGGCTGCTGCTG 1338

Qy 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
 Db 1339 GCTGACTCTCTGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAAACCGGCTC 1398

Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
 Db 1399 AACAAACACATCATGCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCACATGGCC 1458

Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
 Db 1459 TCACACAGAGCTGCTGCTGGGAGAGGAGTGTCTGCACAGACTTCCGATCACAACCATGT 1518

Qy 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
 Db 1519 ATGCAGCTGTGGAAACGATGACAACATGGGATGCTATGGGCTGCTGCTGCTGCTGCTGCT 1578

Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
 Db 1579 ATCCAGAGCGCTGGGTCTCTAGTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1638

Qy 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476

[illegible]

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RESULT 13
US-09-899-471-3
; Sequence 3, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc feature
; LOCATION: (1) - (2022)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-899-471-3

Alignment Scores:
Pred. No.: 6,49e-284 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Indels: 0

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Db 1021 GTNCARGTWSNACNTGGGAARGTNCARYTNCARGCNTGYWSTGCGNGAYWSNTN 1080
Qy 361 GlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeuAsnAsnThrSer 380
Db 1081 GGCNCNTTYAARGAYGATGYTNTGTTGATGARACNGGNTYNAAYAAACWNSN 1140
Qy 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
Db 1141 GTNTGYCNYTNGARCCNWSNGNTGYACCCNTYTCNWSNATGCGNWSNACNMGNGCN 1200
Qy 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTyr 420
Db 1201 GCNMGNTYTCNGGARGARYTNTYTCARGAYTTCNWSNCAAYCATGYATGCARYTNTGG 1260
Qy 421 AsnAspPheAsnMetGlySerLeuTyrAlaCysProMetAspLysTyrIleHisArgArg 440
Db 1261 AAYGAYGAYAAATGGGNSNTYTCGCGTGYCCNATGAYAAATAYATHCAVMGNGN 1320
Qy 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
Db 1321 TGGGTNTGNTGGYTCGNTGYTNTYTCNGCNGCNGNTYNTTYTNTYTYTNTN 1380
Qy 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSer 480
Db 1381 YTNAAARAARGAYMGNMGNAARGCNGMNGNWSNMGNACNGCNYTNTYNTYTCAYWSN 1440
Qy 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
Db 1441 GCNGAYGCGCNGGNTAYGARMGNTYTCGCGTGYCCNATGAYAAATAYATHCAVMGNGN 1500
Qy 501 ProLeuArgValAlaValAspLeuTyrSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
Db 1501 CCNTYTCNGTNGCNGTNGAYTNTGGSNMGNGARGYTNWSNCGNCAYGGGNCNTN 1560
Qy 521 AlaTrpPheHisGlnArgArgArgIleLeuGlnGlyGlyValValIleLeuLeu 540
Db 1561 GCNTGGTTCAYCAYCARMGNGMGNATHTYTCARGARGGNGTNGTNTYNTN 1620
Qy 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
Db 1621 TTYWSNCCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCARACNGTNGARCCN 1680
Qy 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
Db 1681 GGCNCNAYGAYCNYTNGCNGCNGTNGTWSNTGYGTNTYTCNCGAYTTYTNTCARGGN 1740
Qy 581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600
Db 1741 MNGCNCACNGGNTAYGTNGGNTNTAYTYTGAYGNTYNTYTCAYCCNGAYWSNGTN 1800
Qy 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
Db 1801 CCNWSNCCNTTYMGNTGNCNCNTNTYNTYTSNTYTCNACNCARYTNCNCGCNTTYTNTN 1860
Qy 621 AsnAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
Db 1861 GAYCNTYTCARGNGGNTGYWSNACNWSNCGGNGGNCNGCNGAYMGNGTNGARMGN 1920
Qy 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
Db 1921 GTNACNARGCNYTNGWSNCGNTYNGAYWSNTGYACNWSNWSNWSNARGCNGCNGGN 1980
Qy 661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 1981 TGYTGYGARGARTGGGAYTNGGNCNTGYACNACNTNGAR 2022
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RESULT 14

US-10-719-202-3

; Sequence 3, Application US/10719202

; Publication No. US20040121389A1

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

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; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; - PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2022)
; OTHER INFORMATION: n = A,T,C or G
US-10-719-202-3
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Alignment Scores:
Pred. No.: 6,49e-284 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Query Match: 74.0% Indels: 0
DB: 8 Gaps: 0
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US-10-719-202-2 (1-674) x US-10-719-202-3 (1-2022)

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Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 1 ATGCCGTTWSNTGGTYYTNTYNTWSNTGCTYTCNGMGNAAAYCCGCTGCTGCTGCTG 60
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 YTNARGMNTYNTATGARGCCNARGAYACNCGMNGTGYWSNTGCTGCTGCTGCTGCTGCTG 120
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTNAGGAYGGNGAYGTYTNTGYTTCNCGGNSNTYTCARWSNCGCNGCNGCNGCTN 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTNGTCCNACNMGNTNCARACNGARYTNTGNTGYCCNCAARAACNGATGY 240
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 241 GCNTYTCNGTNGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCNGNAARWSNGAYTWSNGARYTNCARGARWSNMGNAAYGCNWSNTYTCARGCNCAR 360
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuValGlnVal 140
Db 361 GTNGTNTYTCNNTTYCARGCNTAYCCNATHGCMNGTGYCCTYTCNTYTCNGTNGCTGCTG 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCNCGCNGAYTNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNTYTCNGCNGARGTNCARATHTGGWSNTAYACNAARCCNMGNTAYACARAARGAR 540
Qy 181 LeuAsnLeuThrGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer 200
Db 541 YTNAAAYTTCNACNARGARYTNCNCGAYGGNGAYAAAYGTNTYTCNACNTYTCNGAYTNG 600
Qy 201 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer 220
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601 GARGARCAGAYTYYWSNTYYTNTAYTTNMGCCNGTCCNGAGCYCNYTNAARWSN 660
 221 LeuTTPYrLyAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 240
 661 YTWGGTAYARAAYTNAACNGCCNCARAAVATHACNYTNAAYCAYACNGAYTTNGTN 720
 241 ProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCys 260
 721 CCNTGYTNTGYATHCARGTGTGWSNYTNGARCCNGAGYWSNGARMGNGTNGARTYTG 780
 261 ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA-gVal 280
 781 CCNTTYTNGARGAYCNGGNGCNCAYMGNAAYTNTGGCAYATHGCMNGNYTNGMGTN 840
 281 LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyIysValThrLeu 300
 841 YTNWSCNGGNGTNTGTCARYTNGAYGCMCCNTGYTTCNGGNAARGTNCACNYT 900
 301 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnLys 320
 901 TGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNYTNGTNCNGCCNGTNCNCARAR 960
 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValIleGlyHisProAsnLeuCys 340
 961 AAYGCNACNGTNAAYGARCNCAGAYTTCARYTNGTNGCNGCNCAYCCNAAYTTNGY 1020
 341 ValGlnValSerThrTrpGluIysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu 360
 1021 GTNCARGTWSNACNTGGARAARGTNCARYTNCARGCNTGYWSNTGGCNGAYWSNYTN 1080
 361 GlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeuAsnThrSer 380
 1081 GGNCCNTTYAARGAYGAYATGYTNTNGTNGARATGAARACNGGNYTNAAYAAVACNWSN 1140
 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
 1141 GTNTGYCNYTNGARCCNWSNGGNTGYACNCCNYTNCNWSNATGCGCWSNACNGGNCN 1200
 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
 1201 GCMNGYTTGGNGARGARYTNTNCARGAYTNTMGWSNCAYCARTGYATGCARYTNTGG 1260
 421 AsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrpIleHisArgArg 440
 1261 AAYGAYCAAAVATGGGNSNYTNTGGCNGTGYCCNATGGAYAAATAYATHCAYMGWGN 1320
 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
 1321 TGGGTNTGTNTGGYTTNGTGYTNTYNTNGCNGCNGCNYTNTYTTTYYTNTYN 1380
 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
 1381 YTNARAARGAYMGNMGNAARGCNGCMGNGWSNMGNCNCTNTNTNTNCAYSN 1440
 481 AlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
 1441 GCNGAYGGGNGGNTAYGARMGNYTNGTNGCNGCNYTNGCNGCNGCNYTNTNCAATG 1500
 501 ProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeu 520
 1501 CCNTYTMGNTGCGTNGAYTNTTGGWSNMGNGMNGARYTNTNSGNCNCAYGNGCNYTN 1560
 521 AlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeuLeu 540
 1561 GCNTGGTGYCAYCAYCARMGNGMNGNATHYTNCARGGNGGNGTNGTNGTNGTNGT 1620
 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
 1621 TTYWSNCCNGCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCARACNGTNGARCCN 1680
 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
 1681 GGNCCNCAYGAYCNYTNGCNGCNGTGGYTNTWSNTGYGTNTYNTNCNGAYTYYTNTCARGN 1740

581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600
 1741 MNGCNCACNGCMGNTAYGTNGGNTTAYTYYGAYGNGTNTYNTCAICCCNGAYWSNGTN 1800
 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
 1801 CCNWSNCCNTTYMGNTGTCNCCTNTTYTWSNTYNTCCNACNCACTYTCNCNGCCTTYTN 1860
 621 AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
 1861 GAYGCNTYTCARGGNGTGYWSNACNWSGNGCNGCMGNCNGAYMGNTGNGARMGN 1920
 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
 1921 GTNACNARGCNYTNGWSNCGTNGAYWSNTGYACNWSNWSNWSNWSNWSNWSNWSNWSN 1980
 661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
 1981 TGYTGYGARGARTGGAYTYTNGCNCCTGYACNACNYTNGAR 2022
 RESULT 15
 US-09-899-471-6
 ; Sequence 6, Application US/09899471
 ; Patent No. US20020146763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Murine Cytokine Receptor
 ; FILE REFERENCE: 00-46
 ; CURRENT APPLICATION NUMBER: US/09/899,471
 ; CURRENT FILING DATE: 2001-07-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Fast-Seq for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 2094
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
 ; OTHER INFORMATION: amino acid sequence of SEQ ID NO:5.
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(2094)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-899-471-6
 Alignment Scores:
 Pred. No.: 1,86e-281 Length: 2094
 Score: 2644.00 Matches: 484
 Percent Similarity: 69.3% Conservative: 0
 Best Local Similarity: 69.3% Mismatches: 190
 Query Match: 73.3% Indels: 24
 DB: 3 Gaps: 1
 US-10-719-202-2 (1-674) x US-09-899-471-6 (1-2094)
 QY 1 MetProValSerTrpPheLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
 Db 1 ATGCCNGTNSWTGGTGTYYTNTYNTWSNTGCTNGCMGNAAYCCNGTNGTNGTNSN 60
 QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 61 YTNARMGNTYNTATGARCNCARGAYACNGCNGMGTGYWSNTYNTGNTYNTNSNTGYCY 120
 QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 121 YTNMGGAYGGNGAYGTNTTGYTTCNGGNGWSNTYNTCARWSNCGCNGCNGCNGT 180
 QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 181 YTNGTTCNACNMGNTYNTCARACNGARYTNGTNTYNTMGNTGYCCNCAARACNGAYGY 240
 QY 81 AlaLeuArgValArgValValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 08:33:35 ; Search time 951 Seconds

(without alignments)
7412.138 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10719202 @CGN 1.1 1147 @runat_16082006_095630_13218 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	2256	6	AAD24220 Murine cy
2	3583	99.4	2328	6	AAD24222 Murine cy
3	3572.5	99.1	2269	15	ABF05372 Mouse zcy

ALIGNMENTS

RESULT 1
AAD24220
ID AAD24220 standard; DNA; 2256 BP.

XX AAD24220;

DT 17-MAY-2002 (first entry)

XX Murine cytokine receptor Zcytor14 DNA.

XX Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
XX gene therapy; protein therapy; gene; ds.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 197..2221

FT /tag= a

FT /product= "Cytokine receptor, Zcytor14"

FT sig_peptide 197..256

FT /tag= b

FT mat_peptide 257..2218

FT /tag= c

FT /product= "Mature cytokine receptor, Zcytor14"

XX WO200204519-A2.

XX

4	3569.5	99.0	2287	15	ABF05376	Aef05376 Mouse zcy
5	3565	98.9	2314	6	AAS18132	Aas18132 Mouse DNA
6	3565	98.9	2314	14	ABF55651	Aef55651 Mouse DCS
7	3562	98.8	2128	6	ABL134982	Ab134982 Murine cd
8	3539	98.2	2331	6	ABK86568	Abk86568 Mouse int
9	2666	74.0	2022	6	AAD24221	Aad24221 Murine cy
10	2644	73.3	2094	6	AAD24223	Aad24223 Murine Zc
11	2637	73.1	2094	6	AAS18133	Aas18133 Mouse DCR
12	2352.5	65.3	2255	4	AAC85027	Aac85027 Human cyt
13	2352.5	65.3	2255	10	AAD47894	Aad47894 Human cyt
14	2352.5	65.3	2255	15	ABF05348	Aef05348 Human IL1
15	2339	64.9	2380	4	AAS46223	Aas46223 Human DNA
16	2339	64.9	2380	4	AAF92138	Aaf92138 Human PRO
17	2339	64.9	2380	4	AAS09515	Aas09515 Human CDN
18	2339	64.9	2380	6	ABF74458	Abf74458 Human CDN
19	2339	64.9	2380	6	ABL88253	Ab188253 Human PRO
20	2339	64.9	2380	6	ABL95742	Ab195742 Human ang
21	2339	64.9	2380	8	ACA89673	ACA89673 CDNA enco
22	2339	64.9	2380	8	ACA73683	ACA73683 Human sec
23	2339	64.9	2380	8	ACA05998	ACA05998 Human sec
24	2339	64.9	2380	8	ACA66832	ACA66832 CDNA enco
25	2339	64.9	2380	8	ACA91244	ACA91244 Novel hum
26	2339	64.9	2380	8	ACD81621	ACD81621 Human CDN
27	2339	64.9	2380	8	ACF20407	ACF20407 Human sec
28	2339	64.9	2380	8	ACF19793	ACF19793 Human sec
29	2339	64.9	2380	8	ACD22081	ACD22081 Human sec
30	2339	64.9	2380	8	ACF13246	ACF13246 Human sec
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45	2339	64.9	2380	8	ACC88420	Acc88420 Human sec

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PD 17-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US021344.
XX
PR 06-JUL-2000; 2000US-021646P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Gao Z;
XX
DR WPI; 2002-179701/23.
DR P-PSDB; AAE14559.
XX
XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
PT receptor, useful for treating inflammation, specifically rheumatoid
PT arthritis, and as educational tools or in research.
XX
PS Claim 8; Page 87-90; 99pp; English.
XX
CC The present sequence is murine cytokine receptor Zcytor14 DNA. The
CC Zcytor14 polypeptide is useful for identifying or isolating Zcytor14
CC ligands, in preparing antibodies, in identifying proteins or peptide
CC cleavage sites, in amino acid sequence analysis, and in monitoring
CC biological activities of both the native and tagged protein in vitro or
CC in vivo. Polypeptides having Zcytor14 activity can be used to treat
CC inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may
CC be used as educational tool in genetics, molecular biology, protein
CC chemistry and antibody production analysis, in the preparation of
CC expression constructs for bacterial, viral or mammalian expression, in
CC determining mRNA and DNA localisation of Zcytor14 polynucleotide in
CC tissues, for identifying related polynucleotides and polypeptides by
CC nucleic acid hybridisation, in linkage-based testing for various diseases
CC in murine models, and to determine whether a subject's chromosomes
CC contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes
CC are useful for in vivo diagnosis, and for detecting and localising
CC Zcytor14 gene expression in tissue samples
XX
SQ Sequence 2256 BP; 416 A; 706 C; 679 G; 455 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,49e-253 Length: 2256
Score: 3605.00 Matches: 674
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-719-202-2 (1-674) x AAD24220 (1-2256)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
DB 197 ATGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 257 CTGGAGAGACTGATGGAGCTCAGACACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
QY 41 LeuTrpAspGlyAspValLeuGluCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 317 CTCTGGATGGTGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 377 CTAGTGCCTTACCGCTGACGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 437 GCCCTCCGNGTCCGNGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgArgAsnAlaSerLeuGlnAlaGln 120
DB 497 GAAAGCTGGAAGACTCTGATTTCAGAACTCCAGGAGTCTAGGAAAGCGCTCTCTCTC 556

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Db 1637 GCGACGAGCGGCTACGAGCGTCTGGTGGAGCACTGGCGTTCGGCCGATG 1696
Qy 501 ProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
Db 1697 CCACTGGCGTGGCGGCGGACCTGTGGAGCGCGCGAGCTGAGCGCGCACGAGCGCTA 1756
Qy 521 AlaTrpPheHisHisGlnArgArgArgGlyLeuGlnGluGlyGlyValValIleLeuLeu 540
Db 1757 GCCTGGTTCACACACGAGCGCGGTATCTTCGAGGAGGTTGGGTGAATCTTCTC 1816
Qy 541 PheSerProAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
Db 1817 TTCTCGCGCGCGCGTGGCGCAGTGTTCAGCAGTGGCTGCAGCTCCAGACAGTGGAGCCC 1876
Qy 561 GlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
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Qy 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
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Qy 621 AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
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Qy 661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2177 TGCTGCGAGGAATGGGACCTGGGACCCCTGCCTACCTACACTAGAA 2218

RESULT 2
ID AAD24222
AD AAD24222 standard; DNA; 2328 BP.
XX
AC AAD24222;
XX
DT 17-MAY-2002 (first entry)
XX
DE Murine cytokine receptor Zcytor14 variant, Zcytor14-1 DNA.
KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW gene therapy; protein therapy; Zcytor14-1; gene; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 197..2293
FT FT /*tag= a
FT FT /product= "Cytokine receptor Zcytor14 variant, Zcytor14-
FT FT 1"
XX
XX WO200204519-A2.
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XX 17-JAN-2002.
XX
XX 05-JUL-2001; 2001WO-US021344.
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XX 06-JUL-2000; 2000US-0216446P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Gao Z;
XX
XX WPI; 2002-179701/23.

```

DR P-PSDB; AAEL4560.

XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
PT receptor, useful for treating inflammation, specifically rheumatoid
PT arthritis, and as educational tools or in research.

PS Claim 8; Page 92-95; 99pp; English.

XX The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
CC polypeptide is useful for identifying or isolating Zcytor14 ligands, in
CC preparing antibodies, in identifying proteins or peptide cleavage sites,
CC in amino acid sequence analysis, and in monitoring biological activities
CC of both the native and tagged protein in vitro or in vivo. Polypeptides
CC having Zcytor14 activity can be used to treat inflammation, such as
CC rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational
CC tool in genetics, molecular biology, protein chemistry and antibody
CC production analysis, in the preparation of expression constructs for
CC bacterial, viral or mammalian expression, in determining mRNA and DNA
CC localisation of Zcytor14 polynucleotide in tissues, for identifying
CC related polynucleotides and polypeptides by nucleic acid hybridisation,
CC in linkage-based testing for various diseases in murine models, and to
CC determine whether a subject's chromosomes contain a mutation in the
CC Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo
CC diagnosis, and for detecting and localising Zcytor14 gene expression in
CC tissue samples. The present sequence is murine Zcytor14 variant, Zcytor14
CC -1 DNA

SQ Sequence 2328 BP; 429 A; 726 C; 702 G; 471 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.29e-252 Length: 2328
Score: 3583.00 Matches: 674
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 0
Query Match: 99.4% Indels: 24
DB: 6 Gaps: 1

US-10-719-202-2 (1-674) x AAD24222 (1-2328)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 197 ATGCTGTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCT 256
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 257 CTGGAGAGACTGATGAGGCTCAGGACACTGACAGCTGTCTCTAGGCTCTCTGCTG 316
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 317 CTCTGGAGTGTGACGTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTG 376
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 377 CTAGTGCCTACCGCTGCAGACGGAGCTGGTGTCTGAGGTGTCCACAGACAGATTGC 436
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 437 GCCTCCGTGTCTGT 496
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 497 GAAGCTGGAAGTCTGATTCAGACTCCAGAGTCTAGGAGCGCTCTCTCCAGGCCAG 556
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 557 GTGGTGTCTCTCTTCCAGGCTTACCCATCGCCGCTGTGTGTGTGTGTGTGTGTGTGT 616
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 617 CCGCTGACCTGT 676
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180

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 Qy 181 LeuAenLeuThrGlnGlnLeuPro----- 188
 Db 737 CTCACCTTACACAGCAGCTGCTGACTGACAGGGGTCTTGAAGTCCGGGACAGATCCAG 796
 Qy 189 -----AapGlyAapAenValLeuLeuThr 196
 Db 797 AGCTGCTGGGTCTGGCCCTGGCTCAATGTGTCTACAGATGGTGACATGCTCTTCTGACA 856
 Qy 197 LeuAapValSerGluGluGlnAapPheSerPheLeuLeuThrLeuA9ProValProAap 216
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 Qy 217 AlaLeuLeuSerLeuThrTyrIlyAenLeuThrGlyProGlnAenIleThrLeuAenHis 236
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 Qy 237 ThrAapLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAapSerGluArg 256
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 Db 1997 TTCCTGCAAGCGCGGCGACCCGCGCTACGTCGGGTCTACTTCGACGGGCTGTGCAC 2056
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 RESULT 3
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 ID AEF05372
 XX AC AEF05372;
 XX DT 23-FEB-2006 (first entry)
 XX DE Mouse zcytoR14 variant cDNA SEQ ID NO 25.
 KW antiinflammatory; antiaathmatic; gastrointestinal-gen.; antiulcer;
 KW antiarthritic; dermatologic; antipsoriatic; antibacterial;
 KW immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
 KW inflammatory bowel disease; asthma; respiratory disease;
 KW ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;
 KW musculoskeletal disease; psoriasis; antipsoriatic;
 KW dermatological disease; immune disorder; atopic dermatitis;
 KW dermatological; endotoxemia; inflammation; endotoxin shock; sepsis;
 KW antibacterial; immunosuppressive; infection; zcytoR14; mutant;
 KW coding sequence; ss.
 XX Mus musculus.
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 XX 29-DEC-2005.
 XX 10-JUN-2005; 2005WO-US020521.
 XX 10-JUN-2004; 2004US-0578805P.
 XX (Zymo) ZYMOGENETICS INC.
 XX Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
 PI

Db	1637	TCCGCGACGGCCTTGCTCCTCCACTCCGCGACGAGCGGGCTACGAGCGTCTGGTGGGA	1699
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Qy	512	ArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgAlaLeu	531
Db	1757	CGCGAGCTGAGCGGCACGCGAGCCCTAGCTGGTTCCACCACGAGCAGCCCGTATCTCTG	1816
Qy	532	GlnGluGlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGln	551
Db	1817	CAGGAGGCTGGCGTGGTAACTCTCTCTCGCCCCGCGCGTGGCGCAGTGTACAGCAG	1876
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Db	1877	TGGCTGAGCTCCAGACAGTGGAGCCCGGCGCATGACGCCCTCGCGCTGGCTCAGC	1936
Qy	572	CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgGlyTrpValGlyValTyrPhe	591
Db	1937	TGCGTGTCTACCCGATTTCTCTCAAGGCGCGCGACCGCGCCTACGTCGGGCTCTACTTC	1996
Qy	592	AspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSer	611
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Qy	612	LeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAla	631
Db	2057	CTGCCCTCGCAGCTCGCGGCTTTCTGTGATGCATGCGAGGAGGCTGCTCCACTTCCGCG	2116
Qy	632	GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSer	651
Db	2117	GGGCGACCCGCGGACCGGGTGGACAGTGCACCCAGCGCTGCGGTCCGCCCTGGACAGC	2176
Qy	652	CysThrSerSerSerGluAlaProGlyCysGluGluTrpAspLeuGlyProCysThr	671
Db	2177	TGTACTTCTAGCTCGGAGCCCGAGGCTGCTCGGAGGAATGGGACCTGGGACCCCTGCCT	2237
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XX	DT	23-FEB-2006 (first entry)	
XX	DE	Mouse zcytor14 variant cdna SEQ ID NO 29.	
XX	KW	antiinflammatory; antiaesthetic; gastrointestinal-gen.; antiulcer;	
XX	KW	antiarthritic; dermatological; antipsoriatic; antibacterial;	
XX	KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;	
XX	KW	inflammatory bowel disease; asthma; respiratory disease;	
XX	KW	ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;	
XX	KW	gastrointestinal disease; arthritis; antiarthritic;	
XX	KW	musculoskeletal disease; psoriasis; antipsoriatic;	
XX	KW	dermatological disease; immune disorder; atopic dermatitis;	
XX	KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;	
XX	KW	antibacterial; immunosuppressive; infection; zcytor14; mutant;	
XX	OS	coding sequence; ss.	
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29-DEC-2005.

10-JUN-2005; 2005WO-US020521.

10-JUN-2004; 2004US-0578803P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
Jaspers SR, Billisborough J;
WPI; 2006-067457/07.
P-PSDB; AEF05377.

New isolated soluble receptor comprises at least one Zcytor14 subunit, useful for treating an inflammatory disease, e.g. asthma, inflammatory bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or psoriasis.

Disclosure; SEQ ID NO 29; 205pp; English.

The invention describes an isolated soluble receptor comprises at least one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ ID NO. 24) given in the specification. Also described are: an isolated soluble receptor comprising Zcytor14, where Zcytor14 comprises a polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces the pro-inflammatory activity of either IL-17A comprising fully defined 153 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153 amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2), and where the antibody or antibody fragment reduces the pro-inflammatory activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16); reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal afflicted with an inflammatory disease in which IL-17A or IL-17F plays a role; and treating a pathological condition in a subject associated with Zcytor14 activity. The soluble receptor comprising at least one Zcytor14 subunit is useful for treating an inflammatory disease, e.g. asthma; chronic inflammatory disease selected from inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or psoriasis; or acute inflammatory disease selected from endotoxemia, septicemia, toxic shock syndrome, or infectious disease. This sequence represents a mouse IL-17A and IL-17F receptor zcytor14 variant.

297 Bp. 410 A: 715 C: 696 G: 466 T: 0 U: 0 Other:

Alignment Scores:	5.96e-251	Length:	2287
Pred. No.:	3569.50	Matches:	671
Score:	97.5%	Conservative:	1
Percent Similarity:	97.4%	Mismatches:	2
Best Local Similarity:	99.0%	Indels:	15
Query Match:	15	Gaps:	1
DBs:			
US-10-719-202-2 (1-674) x AEF05376 (1-2287)			
QY	1	MetProValSerTriPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
DB	197	ATGCCTGTGTCTCTGTTCTCTGTCTGTCTGGCACCTGGCGGAAACCTCTGTGTCGTCTCT	256
QY	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
DB	257	CTGGAGAGACTGATGGAGCCTCAGACACTGCACGCTGCTCTCTAGGCCCTCTCTGCGCAC	316
QY	41	LeuTriPaspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
DB	317	CTCTGGGATGGTGCAGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	376
QY	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIlyThrAspCys	80
DB	377	CTATGTCCTACCCGCTGCAGACGGAGCTGTGTGCTGAGGTGTCACAGAGAAGACAGATTGC	436

PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016767.
XX
PR 24-MAY-2000; 2000US-0206862P.
XX
PA (SCHE) SCHERING CORP.
XX
XX Gorman DM;
XX
XX WPI; 2002-106198/14.
DR P-PSDB; AAU11354.
DR
PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
PT useful for detecting antibodies generated in response to presence of
PT increased protein levels or immunological disorders.
XX
XX Disclosure; Page 17-20; 148pp; English.
XX
XX The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents cDNA encoding the mouse
CC DCRS7 polypeptide
XX
SQ Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: Length: 2314
Score: 3565.00 Matches: 671
Percent Similarity: 96.3% Conservative: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 6 Gaps: 1

US-10-719-202-2 (1-674) x AAS18132 (1-2314)

QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
DB 199 ATGCCTGTCTCTGGTTCTCTGCTGCTTGGCACTGGGCGGAACCTGTGCTCTCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 259 CTGGAGAGACTATGAGAGCTCAGGACACTGCACGCTGCTCTCTAGGCCCTCTCTGCCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 319 CTCTGGAGTGTGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 379 CTAGTGCCTACCGCTCGCAGACGGAGCTGGTGTGCTGAGGTGTCCACAGAGACAGATTGC 438
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 439 GCCCTCTGTGCTGT 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 120
DB 499 GAAGCTGGAAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAACGCCCTCTCTCCAGGCCAG 558
QY 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGlnVal 140
DB 559 GTGGTGTCTCTCTCCAGGCTACCCCATCGCCCGCTGTGCTGTGAGGTGCCAGGTG 618

QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 619 CCCGCTGACCTGGTGCAGCCCTGGTCAAGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 678
QY 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu 180
DB 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGCTCTACACGAAGCCAGGTACCCAGAAAGAG 738
QY 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
DB 739 CTCAACCTCACACAGCAGCTGCCTGACTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
QY 189 -----AspGlyAspAsnValLeuLeuThr 196
DB 799 AGCTGCTGGGTCTGCTCCCTGGCTCAATGTGTCTACAGATGGTGACAATGCTCTTCTGACA 858
QY 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp 216
DB 859 CTGGATGCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTGCTGCTGCTGCTGCTGCTGCTG 918
QY 217 AlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
DB 919 GCTCTCAATCTCTGTGGTACAAAACCTGACTGGACCTCAGAACATTAATTCTTTAAACAC 978
QY 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
DB 979 ACAGCTCTGGTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
QY 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
DB 1039 GTCGAAATCTGCTCCCTCTCCGGGAAGATCCCGGTGCACACAGGAACCTCTTGCCACATAGCC 1098
QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
DB 1099 AGGCTGCGGGTACTGTCTCCAGGGGTATGGCAGCTAGTAGTGGCTTGTGTCTGCTGCTGCTG 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
DB 1159 AAGGTAACTCTGTGCTGGCAGCCACAGACCCAGAGTCTCTGCCAGCCACTTGTGTCACCA 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
DB 1219 GTGCCCCAGAAAGACGCCACTGTGAATGAGCCACCAAGATTTCAGATTGCTGGTGGCAGCCAC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
DB 1279 CCCAACCTCTGTGTCCAGTGGACACTGGGAGAGGTTCAAGTGAAGCGTGTGTGTGG 1338
QY 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
DB 1339 GCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGTGTAGTGGAGATGAAACCGGCCCTC 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
DB 1399 AACAAACATCATGCTGTGCTTGGAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
DB 1459 TCCACAGAGCTGTCTCGCTGGGAGGAGGTGTGCTGCAAGACTTCCGATCACACAGTGT 1518
QY 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrp 436
DB 1519 ATGCAGCTGTGGAACGATGACAACTGGGATCGCTATGGGCTGCCCCATGGACAGATAC 1578
QY 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaAlaLeuPhe 456
DB 1579 ATCCACAGCGCTGGTCTCTAGTATGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1638
QY 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
DB 1639 TTTCTTCTCTCTTAAAAAAGGACCGCAGGAAGCGGCCCGTGGCTCCCGCAGCGGCTTG 1698
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeuAlaSerAla 496

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Db 1699 CTCCTCCACTCCGCGCAGCGGCTACGAGCGCTGGTGAGCACTGGCGTCCGCG 1758
Qy 497 LeuSerGlnMetProLeuArgValAlaValAapLeuTrpSerArgGluLeuSerAla 516
Db 1759 TTGAGCCAGTCCACTGCGCGTGGCCGCGGACCTGTGAGCGCGCGGAGCTGAGCGG 1818
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgileLeuGlnGluGlyVal 536
Db 1819 CACGAGCCCTAGCCTGTTCCACCACAGCAGCGCGTATCTGCGAGGAGGTGGCGTG 1878
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeu 556
Db 1879 GTAATCCTTCTCTCTCGCCCGCGCGTGGCGCGAGTGTGAGCAGTGGCTGCAGTCCAG 1938
Qy 557 ThrValGluProGlyProHisAapAlaLeuAlaTrpLeuSerCysValLeuProAap 576
Db 1939 ACAGTGGAGCCCGCGCGCATGACGCCCTGCGCGCTGGCTGAGCTGCTGCTACCCGAT 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValGlyPheAapGlyLeuLeuHis 596
Db 1999 TTCCTGCAAGCGCGGCGGACCGCGCTACGTGGGGTCTATTTCGACGGGTGCTGCAC 2058
Qy 597 ProAapSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCCCTCCCGTTCGCGTGGCGCGCTCTCTCCCTGCGCTCGCAGCTG 2118
Qy 617 ProAlaPheLeuAapAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAap 636
Db 2119 CCGGCTTTCTCGTGGATGCACTGACGAGGAGCTCTCCACTTCCGCGGGCGACCCGCGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAapSerCysThrSerSerSer 656
Db 2179 CGGTGGACGAGTGAACCCAGCGCTGCGGTGCGCTGCGACGCTGACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysGluGluTrpAapLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGTGCGAGGAATGGGACCTGGGACCCCTGCACTACACTAGAA 2292
RESULT 6
AEB55651
ID AEB55651 standard; cDNA; 2314 BP.
AC AEB55651;
DT 22-SEP-2005 (first entry)
DE Mouse DCSR7 polypeptide encoding cDNA.
KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
KW DCSR8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
KW interstitial lung disorder; asthma; allergy; atherosclerosis;
KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
KW antipsoriatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
KW antiulcer; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
KW IL-17C agonist; mouse; DCSR7; gene; ss; antisense therapy; RNAi therapy.
OS Mus musculus.
FH Key
FT CDS Location/Qualifiers
FT 199..2295
FT /*tag= C
FT /product= "DCSR7"
FT mat_peptide 199..2292
FT /*tag= b
FT sig_peptide 199..258
FT /*tag= a
XX WO2005065711-A2.
XX 21-JUL-2005.
XX 22-DEC-2004; 2004WO-US042935.

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XX 29-DEC-2003; 2003US-00749144.
PR (SCHE ) SCHERING CORP.
PA Gorman DM;
XX WPI; 2005-506792/51.
DR P-PSDB; AEB55652.
XX Modulating activity of cell, involves contacting cell with an agonist or
PT antagonist of DNAX cytokine receptor subunit.
XX Example 5; SEQ ID NO 7; 130pp; English.
XX The invention relates to modulating (M1) activity of cell, by contacting
CC cell with an agonist or antagonist of DNAX cytokine receptor subunit
CC (DCSR9) or of interleukin (IL)-17C where the cell modulates psoriasis,
CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
CC the disorders which involves administration of the modulator and
CC diagnosing (M3) a disorder as mentioned above that involves contacting a
CC sample from a test subject with a binding composition that specifically
CC binds to a polypeptide or nucleic acid of DCSR9 or IL-17C. (M1) is useful
CC for modulating an activity of a cell. (M2) is useful for treating a
CC subject suffering from a disorder such as psoriasis, IBD, interstitial
CC lung disorder, asthma or allergy, or atherosclerosis, where the
CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
CC granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
CC ulcerative colitis. The present sequence represents a mouse DCSR7
CC polypeptide encoding cDNA.
XX SQ Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2314
Score: 3565.00 Length: 2314
Percent Similarity: 96.3% Matches: 671
Best Local Similarity: 96.1% Conservative: 1
Query Match: 98.9% Mismatches: 2
DB: 14 Indels: 24 Gaps: 1

US-719-202-2 (1-674) x AEB55651 (1-2314)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAapProValValSer 20
Db 199 ATGCTGTGTCTCTGTGTCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTCT 258
Qy 21 LeuGluArgLeuMetGluProGlnAapThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGGAGGCTCAGGACACTGCACGCTGTCTCTAGGCTCTCTGTGCCAC 318
Qy 41 LeuTrpAapGlyAapValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCGGATGGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 378
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnYsThrAapCys 80
Db 379 CTAGTGCCTTACCCGCTGCAGACGAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCCTCTGTGTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
Qy 101 GluAlaGlyLeuSerAapSerGluLeuGlnGlnSerArgAapAlaSerLeuGlnAlaGln 120
Db 499 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTTAGGAACGCTCTCTCCAGGCCAG 558
Qy 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGlnVal 140
Db 559 GTGGTGTCTCTCTCCAGGCTTACCCATCGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGT 618
Qy 141 ProAlaAapLeuValGlnProGlyGlnSerValGlySerAlaValPheAapCysPheGlu 160

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Db 619 CCCGCTGACCTGGTGGACGCCCTGAGTCCGCTGGGTTCTCGGGTATTTGACTGTTTCGAG 678
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTTACACAGAACCCAGGTACAGAAAGAG 738
Qy 181 LeuAenLeuThrGlnGlnLeuPro----- 188
Db 739 CTCACCTCACACAGCAGCTGCTGACTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 799 AGCTGCTGGGTCTGCTCCCTGGCTCAATGTGTCTACAGATGGTGACAATGCTCTTCTGACA 858
Qy 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTCGCTCCAGTCCCGGAT 918
Qy 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 919 GCTCTCAATCTTGTGTGTCACAAAACCTGACTGGACCTCAGAACATTACTTTAAACACAC 978
Qy 237 ThrAspLeuValProCysLeuGlnValTrpSerLeuGluProAspSerGluArg 256
Db 979 ACAGACCTGGTTCCTGCTCTGCATTCAGGTGTGGTCTGCTAGGCCAGACTCTGAGAGG 1038
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 1039 GTCGAATTCGCCCTTCGGGGAGATCCCGTGCACACAGAACCTCTGGCACATAGCC 1098
Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysLeuProGly 296
Db 1099 AGGCTGCGGGTACTGTCCCAAGGGGTATGGCAGCTAGATGGCCCTGTCTGTCTGCGCGGC 1158
Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTAACTGTGTGGCAGGCACACAGAGTCCCTGCCAGCCACTTGTGCCACCA 1218
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAAAGACGCCACTGTGAATGAGCCACAAAGATTTCCAGTTGTGTGGCAGGCCAC 1278
Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1279 CCCAACCTCTGTGTCCAGTGAGCACCTGGGAGAGGTTCAGCTCAAGCGTGTGTGG 1338
Qy 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGTGTAGTGGAGATGAAAACCGGCTC 1398
Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACACACATCAGTCTGTGCCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
Qy 397 SerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCCACGAGAGCTGTGCTGGGAGGAGGTGTCTGCAAGACTTCGATTCACACACAGTGT 1518
Qy 417 MetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
Db 1519 ATGCAGCTGTGAACGATGACAACTGGATCGCTATGGCCCTGCCCATGACAAAGTAC 1578
Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1579 ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTGCTACTCTTGGCTGCGGCGCTTTTC 1638
Qy 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1639 TTCCTTCTCTTAAAGAGACCGCAGGAAGCGGCCCGTGGCTTCCCGCACGCGCTTTG 1698
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496

Db 1699 CTCCTCCACTCCGCGCAGGAGCGGCTACGAGCGCTGTGGGAGCACCTGGCGTCCGCG 1758
Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
Db 1759 TTGAGCCAGATGCCACTGCGGTGGCGGTGAGCCCTGTGTGAGCCGCGGAGCTGAGCGCG 1818
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyVal 536
Db 1819 CACGAGGCCCTAGCTGTGTTCCACACACAGCGACGCCGTATCTCTGACGAGGGTGGCGTG 1878
Qy 537 VallIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1879 GTAATCTTCTTCTTCTGCGCGCGCGCTGCGCGAGTGTACAGCAGTGGCTGCAGCTCCAG 1938
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
Db 1939 ACAGTGGAGCCCGGCGCGCATGACGCCCTCGCGCGCTGCTCAGCTGTGTCTACCCGAT 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1999 TTCCTGCAAGCCCGGCGACCGCGCGCTACGTGGGGTCTACTTCGACGGGCTGTGCAC 2058
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCCCTCGCGCTCGCGCTCGCGCTCTTCTCTCCCTGCGCTCGAGCTG 2118
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTTCCTGGATGCACTGCAGGAGGCTCTCCACTTCGCGGGCGGACCCCGGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACAGTGAACCCAGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGTGTCAGGAATGGGACCTGGGACCTGCACCTACACTAGAA 2292
RESULT 7
ABL34982
ID ABL34982 standard; cDNA; 2128 BP.
XX ABL34982;
AC ABL34982;
XX 04-APR-2002 (first entry)
DT Murine cDNA isolated from skin cells SEQ ID NO: 487.
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.
XX Mus sp.
XX WO200190357-A1.
XX 29-NOV-2001.
XX 24-MAY-2001; 2001WO-NZ0000099.
XX 24-MAY-2000; 2000US-0206650P.
PR 25-JUL-2000; 2000US-0221232P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA Watson JD, Strachan I, Sleeman M, Onrust R, Murison JG;
PI Kumble KD;
XX WPI; 2002-122020/16.
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,

PT growth and developmental defects, inflammatory diseases, or for PT modulating immune responses.

PS Claim 1: Page 295: 466pp: English.

The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.

Sequence 2128 BP: 387 A; 674 C; 626 G; 441 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,928-250	Length:	2128
Score:	3562.00	Matches:	670
Percent Similarity:	96.3%	Conservative:	2
Best Local Similarity:	96.0%	Mismatches:	2
Query Match:	98.8%	Indels:	24
DB:	6	Gaps:	1

US-10-719-202-2 (1-674) x ABL34982 (1-2128)

Qy	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAenProValValValSer	20
Db	1	ATGCGTGTCTCTGGTTCTGCTGCTTGGCACTGGCGCGAAACCCCTGTGGTCTCT	60
Qy	21	LeuGluAtrGLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	61	CTGGAGAGACTGATGAGGCTCAGACACTGCACGTCTCTTAGGCGCTCTCTCGCCAC	120
Qy	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	121	CTCTGGATGGTGACGTGCTCTGCTGCTGGAGCCCTCAGTCTGCCCGCAGCCCTGTG	180
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
Db	181	CTAGTGCCTACCGCGCTGCAGACGAGCTGGTGTCTGAGTGTCCACAGAAGACAGATTGC	240
Qy	81	AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
Db	241	GCCTCTGTGTCCTGGTGGTGCTGCACATTGGCCGTCATGGCGACTGGCGAGAGCCTGAA	300
Qy	101	GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAenAlaSerLeuGlnAlaGln	120
Db	301	GAAGCTGGAAAGCTCTGATTCAAACTCCAGGAGCTAGGAACGGCTCTCTCCAGGCCAC	360
Qy	121	ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal	140
Db	361	GTGTGTCTCTCCTTCAGGCGCTTACCCCATCGCCCGCTGTGCTGTGGAGGTCAGGTG	420
Qy	141	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
Db	421	CCCGCTGACCTGGTGAGCGCTGGTCAGTCCGTTGGGTCTTGGGGATTTTGACTGTTTCGAG	480
Qy	161	AlaSerLeuGlyAlaGluValGlnIleTrpSerTyThrLysProArgTyGlnLysGlu	180
Db	481	GCTAGTCTTGGGCTGAGGTACAGATCTGGTCTCTACAGAGCCCGAGTACCAGGAAGAG	540
Qy	181	LeuAsnLeuThrGlnGlnLeuPro-----	188
Db	541	CTCAACCTCACAGCAGCTGCTGACTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAG	600
Qy	189	-----AspGlyAspAenValLeuLeuThr	196
Db	601	AGCTGCTGGGTCTCGCCCTGGCTCAATGTGTCACAGATGGTGACAATGTCCCTTCGTACA	660
Qy	197	LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp	216


```
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTCTCTCAAGCCGGCGACCGCGCTACCTCGGGGTCTACTTCGACGGGCTGTCGAC 1860

Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCAGACTCTGTGGCCCTCCCGGTCCGGCTCGCCCGCTCTTCTCCCTGCGCTCGAGCTG 1920

Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCGGCTTCTTGGATGCACTGACGGAGGCTGCTCCACTTCGGCGGGCGACCCGCGAC 1980

Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 1981 CCGGTGGAAACAGTACACCGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTACCTCG 2040

Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GAAGCCCCAGGCTGCTCGGAGAAATGGACCTGGGACCTCGACTACACTAGAA 2094

RESULT 8
ABK86568
ID ABK86568 standard; cDNA; 2331 BP.
AC ABK86568;
XX
XX
XX 24-SEP-2002 (first entry)
XX
XX Mouse interleukin 17 receptor like protein, IL-17RL, full length cDNA.
XX
XX Mouse; ss; gene; Interleukin 17 receptor-like protein; IL-17RL;
KW chondrocyte; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteopathic; antirheumatic; antiarthritic; relapsing polyarthrit;
KW seronegative spondyloarthropathy; bone morphogenetic protein.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH 199. .2295
CDS /*tag= a
FT /*product= "IL-17RL"
FT /transl_except= (pos:2077. .2079,aa:Xaa)
FT /transl_except= (pos:2161. .2163,aa:Xaa)
FT /transl_except= (pos:2200. .2202,aa:Xaa)
FT /transl_except= (pos:2242. .2244,aa:Xaa)
FT /note= "Xaa is unknown"
XX
XX WO200238764-A2.
XX
XX 16-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US043855.
XX
XX 10-NOV-2000; 2000US-0247134P.
XX 23-FEB-2001; 2001US-0271197P.
XX 12-OCT-2001; 2001US-0328904P.
XX
XX (REG ) UNIV CALIFORNIA.
XX
XX Haudenschild D, Rose L, Moseley T, Reddi AH;
XX
XX WPI; 2002-508211/54.
XX P-PSDB; AAU99161.
XX
XX Interleukin-17 receptor-like polypeptide useful for the manufacture of a
XX medicament to modulate cartilage or bone growth in a mammal.
XX
XX Claim 84; Page 88-89; 108pp; English.
XX
XX The invention relates to an interleukin-17 receptor-like (IL-17RL)
XX
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CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-
CC 17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included
CC are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic
CC host cells, a method of determining the aggressiveness of a prostate
CC cancer cell, by determining the presence or absence in the cell of a
CC group of IL-17RL (where the determination that the group is absent in the
CC cell indicates that the cancer is more aggressive than a like cell in
CC which the group is present) and a mammalian cell comprising a
CC polynucleotide encoding an IL-17B antagonist, where the cell is selected
CC from chondrocyte, synovioocyte, and mesenchymal stem cell. IL-17RL or the
CC polynucleotide is useful for the manufacture of a medicament to modulate
CC cartilage or bone growth in a mammal. The polynucleotide is useful for
CC the manufacture of a medicament to restore androgen-responsiveness to a
CC prostate cancer cell. IL-17RL is useful for decreasing catabolic activity
CC in bone or cartilage in a mammal. IL-17RL is useful for inhibiting
CC ossification or calcification in a mammal suffering from pathological
CC ossification or calcification, for diagnosing a cartilage degenerative
CC disorder in a mammal, for inhibiting the rate of proteoglycan synthesis
CC by a chondrocyte in culture, and for the manufacture of a medicament to
CC potentiate the activity of a bone morphogenetic protein in a mammal. An
CC IL-17RL antagonist is useful for treating a bone or cartilage pathology
CC such as a degenerative cartilage disorder selected from osteoarthritis,
CC rheumatoid arthritis, relapsing polyarthrit, allergic skin immune response
CC spondyloarthropathies, multiple sclerosis, and organ transplant rejection. IL-17RL is particularly a receptor for IL
CC and organ transplant rejection. IL-17RL is particularly a receptor for IL
CC -17B (chondrocyte, a proinflammatory cytokine). The gene for IL-17RL is
CC located on chromosome 3p25.3-3p24.1. The present sequence is the full
CC length cDNA sequence for mouse IL-17RL
XX
```

SQ Sequence 2331 BP; 428 A; 725 C; 695 G; 473 T; 0 U; 10 Other;

Alignment Scores: 1.03e-248 Length: 2331
Pred. No.: 3539.00 Matches: 666
Score: 95.6% Conservative: 1
Percent Similarity: 95.4% Mismatches: 7
Best Local Similarity: 98.2% Indels: 24
Query Match: 6 Gaps: 1
DB:

US-10-719-202-2 (1-674) x ABK86568 (1-2331)

```
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 199 ATGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258

Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGGAGCCTCAGGACACTGACACCTGCTCTCTAGGCTCTCTGCCCAC 318

Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCTGGGATGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378

Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIlyThrAspCys 80
Db 379 CTAGTGCCTACCCGCTGCAGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438

Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCCTCTGTGTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498

Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 499 GAAGCTGGAAAGTCTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG 558

Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 559 GTGGTGTCTCTCTCTCAGGCTTACCCATCGCCGCTGTGTGTGTGTGTGTGTGTGTGT 618

Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 619 CCCGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678
```

Qy 161 AlaSerLeuGlyAlaGluValGlnIleTyrSerTyrThrLysProArgTyrGlnLysGlu 180
Db 679 GCTAGTCTGCGGCTGAGGTACAGATCTGGTCTTACACGAAGCCAGGTACCAAGAGAG 738
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 739 CTCACCTTCACACAGCAGCTGCCCTGACTGTCAGGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 799 AGCTGCTGGGTCCCTGGCTCAATGTGTCTACAGATGGTGACATGTCTTCTGACA 858
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGATGCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTGCGTCCAGTCCCGAT 918
Qy 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 919 GCTCTCAAAATCTTGTGTGTAACAAACCTGACTGGACCTCAGAAACATTTACTTTAAACAC 978
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTyrSerLeuGluProAspSerGluArg 256
Db 979 ACAGACTGTCTCCCTGCTGCAATTCAGGTGTGTGCTAGAGCCAGACTCTGAGAGG 1038
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTyrPheIleAla 276
Db 1039 GTCGAATTCCTGCCCTCCGGGAAGATCCGGTGCACACAGGAACCTCTGGCACAATAGCC 1098
Qy 277 ArgLeuArgValLeuSerProGlyValTyrGlnLeuAspAlaProCysCysLeuProGly 296
Db 1099 AGGCTGGGGTACTGTCCCGAGGGGTATGGCAGCTAGATGGCCCTTGTCTGTCCGGGC 1158
Qy 297 LysValThrLeuCysTyrGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTACACTGTCTGGCAGGACACGACGAGTCCCTGCCAGCCACTTGTGGCACCA 1218
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAAAGACGCCACTGTGAATGAGCCACAGATTTCCAGATTGTGGTGGCAGGCCAC 1278
Qy 337 ProAsnLeuCysValGlnValSerThrTyrGluLysValGlnLeuGlnAlaCysSerTyr 356
Db 1279 CCCAACCTCTGTGTCCAGGTGAGCACCTGGGAGAAGGTTTCAGCTGCAAGGCTGTGTGTGG 1338
Qy 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGCCCTTCAAGGATGATGCTGTGTAGTGGAGATGAATAACCGGCTC 1398
Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACCAACATCAGTCTGTGCTTGGNAACCCAGTGGCTGTACACCACTGCCAGCATGCC 1458
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCCACGAGAGTGTGCTGCCCTGGGAGAGAGTGTGTCAGAGATTTCCGATCACACCAAGTGT 1518
Qy 417 MetGlnLeuTyrAsnAspAsnMetGlySerLeuTyrAlaCysProMetAspLysTyr 436
Db 1519 ATGCACTGTGGAAACGATGACAACTGGGATGCGTATGGGCTGCCCCATGGACAGATAC 1578
Qy 437 IleHisArgArgTyrValLeuValTyrLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1579 ATCCACAGCGCTGGTCTTAGTATGCTGGCTGCTGCTTCTTGGCTGGCGCTTTTC 1638
Qy 457 PhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1639 TTCTTCTCTCTTCAAAAAGGACCGCAGGAAGCGGCGCTGCTCCCGCAGCGCTTG 1698
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1699 CTCTTCACCTCCGCGCAGGAGCGGGCTACAGCGCTGTGGGAGCAGCTGGCGTCCGG 1758

Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTyrSerArgArgGluLeuSerAla 516
Db 1759 TTGAGCCAGATGACCTGCGCGTGGCGTGGACCTGTGGAGCCGCCGAGCTGAGCGCG 1818
Qy 517 HisGlyAlaLeuAlaTyrPheHisHisGlnArgArgIleLeuGlnGlyGlyVal 536
Db 1819 CAGGAGCCCTAGCTGTGTTCACACACGAGAGCGGTATCTTCAGAGAGGGTGGGTG 1878
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTyrLeuGlnLeuGln 556
Db 1879 GTAATCCTTCTCTCTCGCCCGCGCGTGGCGAGTGTTCAGCAGTGGCTGCAGCTCCAG 1938
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTyrLeuSerCysValLeuProAsp 576
Db 1939 ACAGTGGAGCCCGCGCGCATGACGCCCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuHis 596
Db 1999 TTCCTGCAAGCCGGCGGACCGCGCTACGTGGGTCTACTTCGACGGGCTGCTGCAC 2058
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCGCTCCCSSTTCGGGTGCGCGCTCTTCTCCCTGCGCTCGCAGCTG 2118
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTTCCTGGATGCACTGACAGGAGGCTGCTCCACTTCCCGGGCGGACCGCGGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACAGTGAACCCAGSCSTGCGGTGCCCTGACAGCTGTACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysCysGluGluTyrAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAASCCCGAGCTGCTGGAGGATGGACCTGGACCTGCACACTACACTAGAA 2292

RESULT 9
AAD24221
ID AAD24221 standard; DNA; 2022 BP.
XX
AC AAD24221;
XX
DT 17-MAY-2002 (first entry)
XX
DE Murine cytokine receptor, Zcytor14 degenerate DNA.
XX
KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW gene therapy; protein therapy; ds.
XX
OS Mus sp.
XX
PN WO200204519-A2.
XX
PD 17-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US021344.
XX
PR 06-JUL-2000; 2000US-0216446P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gao Z;
XX
DR WPI; 2002-179701/23.
XX
PT New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
PT receptor, useful for treating inflammation, specifically rheumatoid
PT arthritis, and as educational tools or in research.
XX
PS Claim 8; Page 92; 99pp; English.
XX
CC The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
CC polypeptide is useful for identifying or isolating Zcytor14 ligands, in

CC preparing antibodies, in identifying proteins or peptide cleavage sites,
CC in amino acid sequence analysis, and in monitoring biological activities
CC of both the native and tagged protein in vitro or in vivo. Polypeptides
CC having Zeytor14 activity can be used to treat inflammation, such as
CC rheumatoid arthritis. Zeytor14 polynucleotide may be used as educational
CC tool in genetics, molecular biology, protein chemistry and antibody
CC production analysis, in the preparation of expression constructs for
CC bacterial, viral or mammalian expression, in determining mRNA and DNA
CC localisation of Zeytor14 polynucleotide in tissues, for identifying
CC related polynucleotides and polypeptides by nucleic acid hybridisation,
CC in linkage-based testing for various diseases in murine models, and to
CC determine whether a subject's chromosomes contain a mutation in the
CC Zeytor14 gene. Zeytor14 oligonucleotide probes are useful for in vivo
CC diagnosis, and for detecting and localising Zeytor14 gene expression in
CC tissue samples. The present sequence is a degenerate form of DNA encoding
CC murine cytokine receptor, Zeytor14 (AAE14559)
XX
SQ Sequence 2022 BP; 240 A; 248 C; 377 G; 272 T; 0 U; 885 Other;

Alignment Scores:
Pred. No.: 5,286-185 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Query Match: 74.0% Indels: 0
DB: 6 Gaps: 0

US-10-719-202-2 (1-674) x AAD24221 (1-2022)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 1 ATGCCNGTNSNTGGTYTNTYNTNSNTGNGTNGGNGMAAYCCNGTNGTNGTNSN 60
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 YTGARGMGNTYATGGARCCNCARGAAYACNGCMGNTGWSNYTNGGNTNSNGTCAY 120
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTTGGGAYGGGAYGTNTYNTGYTNCNGGWSNYTNCARWSNGCNCNGCNGCNGT 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTTGTTCCNACMGNTNCARACNGARYTNGTNTGNTGNGTNCAYGNGCAYTGGCGNGARCCNGAR 300
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 241 GCNTTNGGNTNGTNGTNGTNCAYTNGCNGTNCAYGNGCAYTGGCGNGARCCNGAR 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCGNNAARWSNGAYWSNGARYTNCARGARWSNMGNAAYGCNWSNTYTCARGCNCAR 360
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 361 GTTGTNTYNTNSNTTYCARGCNTAYCCNATGCGNWTGTCGNTYNTNGTNGTNCARGT 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCNCGCAYTNGTNCARCCNGCNGCARWSNGTNGGWSNGCNGTNTTYGATGYTTYGAR 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNTYNTGNGCNGARGTNCARATHGGSNTAYACNARCCNMGNTAYCABAARGAR 540
Qy 181 LeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuLeuLeuValSer 200
Db 541 YTNAAAYTNCARCACTYTCNCGAYGNGGAYAAAGTNTYNTNACNTYNTNGAYGTWSN 600
Qy 201 GluGlnGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer 220
Db 601 GARGARCARGAYTNTYNTYNTYNTYNTYNTYNTYNTYNTYNTYNTYNTYNTYNTYNT 660

Qy 221 LeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 240
Db 661 YTTTGGTAYAAARAAAYTTNACNGCNCARAAAYTHACNTYNTAAAYCAVACNGAYTTNGTN 720
Qy 241 ProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCys 260
Db 721 CCNTGYTNTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 261 ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuVal 280
Db 781 CCNTTYMGNGARGAYCCNGCNGCNCAYMGNAAYTNTGTCAYATGCGNMGNTYNTMGNGTN 840
Qy 281 LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 300
Db 841 YTNWSNCCNGGNGTNGGTCARNTYNGAYGNCNCNTGYTYTTCNCGGNAARGTACNCTN 900
Qy 301 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProValProGlnLys 320
Db 901 TGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNTYNTGTCNCCNGTNCNCARAA 960
Qy 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
Db 961 AAYGCNACNTNAAAYGARGCNCARGAYTTCARYTGTGTGTCGNGCNCAYCCNAAAYTNTGY 1020
Qy 341 ValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu 360
Db 1021 GTNCARGTNSNACNTGGGARAARGTNCARYTNCARGCNTGYWSNTGGCGNGAYWSNTN 1080
Qy 361 GlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSer 380
Db 1081 GGNCNTTYAARGAYGATGYTNTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
Db 1141 GTNTGYGNTYNGARCCNWSNGGNTGYACNCCNTYTCNWSNATGGCNSNACNMGNGCN 1200
Qy 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
Db 1201 GCNMGNTYNGCNGARGARYTNTYNTNCARGAYTYTNGWSNCACTGATGATGATGATGAT 1260
Qy 421 AsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg 440
Db 1261 AAYGAYGAYAAAYATGGGWSNYTNTGGCNGTGYCCNATGGAYAAATATATATATATAT 1320
Qy 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePhePheLeuLeu 460
Db 1321 TGGTNTYNTGNTGTYTNGCNGCNGTGYTNTYNTYNTYNTYNTYNTYNTYNTYNTYNT 1380
Qy 461 LeuLysLysAspArgArgGlyAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
Db 1381 YTNAAARARGAYMGNGNAARGCNCNMGNGWSNMGNAACNCGNTYNTYNTYNTYNTYNT 1440
Qy 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
Db 1441 GCNGAYGNGCNGGNTAYGARGMNTGTGNGCNGTNGCNGCNGTNGCNGCNGTNGCNGC 1500
Qy 501 ProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeu 520
Db 1501 CCNTYNTMGNTGTCNGTNGAYTNTGGWSNMGNGARGARYTNGWSNCGCAYGNGCNGT 1560
Qy 521 AlaTrpPheHisGlnArgArgGlyLeuGlnGluGlyGlyValValValLeuLeu 540
Db 1561 GCNTGTTTTCAYCAYCARMGNGMGNAATHTYTCARGARGGNGTNGTNGTNGTNGTNGT 1620
Qy 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
Db 1621 TTWSNCCNGCNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNGCNG 1680
Qy 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
Db 1681 GGNCNCAYGNCNTGNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNGCNGTNG 1740
Qy 581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600

Db 1741 MGNCGNACNGMNTAYGTNGGNGTNTAVTYYGAYGNTYNTNCAYCCNGAYWSNGTN 1800
 Qy 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
 Db 1801 CCWNSCCTTYMGNGTNGCNGCTNTTYSNTYNTCCNACNARYTNCNGCNGTNTTYYN 1860
 Qy 621 AspAlaLeuGlnGlyGlyCySerThrSerAlaGlyArgProAlaAspArgValGluArg 640
 Db 1861 GAYGNTYNTCARGGNGGNTGYWSNACNWSNGCNGNGCNGCNGAYMGNGTNGARMGN 1920
 Qy 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
 Db 1921 GTNACNARGCNYTNGMNGCNGCTNTGAYWSNTGYACNWSNWSNGARGCNGCNGGN 1980
 Qy 661 CysCysGluGluTTPAspLeuGlyProCysThrThrLeuGlu 674
 Db 1981 TGYTGARGARTGGGAYTNGGNCCTGYACNACNTNGAR 2022
 RESULT 10
 ID AAD24223 standard; DNA; 2094 BP.
 XX AAD24223;
 AC AAD24223;
 XX 17-MAY-2002 (first entry)
 XX Murine Zcytor14 cytokine receptor variant, Zcytor14-1 degenerate DNA.
 DE Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
 KW gene therapy; protein therapy; Zcytor14-1; ds.
 KW
 XX Mus sp.
 XX W0200204519-A2.
 FN 17-JAN-2002.
 XX 05-JUL-2001; 2001WO-US021344.
 XX 06-JUL-2000; 2000US-0216446P.
 PR (ZYMO) ZYMOGENETICS INC.
 XX Gao Z;
 XX WPI; 2002-179701/23.
 DR New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
 PT receptor, useful for treating inflammation, specifically rheumatoid
 PT arthritis, and as educational tools or in research.
 XX Claim 8; Page 97-98; 99pp; English.
 PS The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
 CC polypeptide is useful for identifying or isolating Zcytor14 ligands in
 CC preparing antibodies, in identifying proteins or peptide cleavage sites,
 CC in amino acid sequence analysis, and in monitoring biological activities
 CC of both the native and tagged protein in vitro or in vivo. Polypeptides
 CC having Zcytor14 activity can be used to treat inflammation, such as
 CC rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational
 CC tool in genetics, molecular biology, protein chemistry and antibody
 CC production analysis, in the preparation of expression constructs for
 CC bacterial, viral or mammalian expression, in determining mRNA and DNA
 CC localisation of Zcytor14 polynucleotide in tissues, for identifying
 CC related polynucleotides and polypeptides by nucleic acid hybridisation,
 CC in linkage-based testing for various diseases in murine models, and to
 CC determine whether a subject's chromosomes contain a mutation in the
 CC Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo
 CC diagnosis, and for detecting and localising Zcytor14 gene expression in
 CC tissue samples. The present sequence is a degenerate form of DNA encoding
 CC murine Zcytor14 variant, Zcytor14-1 (AAE14560)

SQ Sequence 2094 BP; 248 A; 252 C; 393 G; 283 T; 0 U; 918 Other;
 Alignment Scores:
 Pred. No.: 2,23e-183 Length: 2094
 Score: 2644.00 Matches: 484
 Percent Similarity: 69.3% Conservative: 0
 Best Local Similarity: 69.3% Mismatches: 190
 Query Match: 73.3% Indels: 24
 DB: 6 Gaps: 1
 US-10-719-202-2 (1-674) x AAD24223 (1-2094)
 Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
 Db 1 ATGCCNGTNSNTGGTYYTNTYNTWSNTGCTNTGNGMNAAYCCNGTNGTNGTNSN 60
 Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 61 YTNGARMGNTYNTATGGARCNCARGAYACNGCMGNTGYWSNTGNGTNTWSNTGYCAY 120
 Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 121 YTNNGGAYGGNGAYGTNTNTGYTNCNGGWSNTYTCARWSNCCNGCNGCNGTN 180
 Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 181 YTNGTNCCNACNMGNTYTCARACNCGARYTNGTNTYTMGNTGYCCNARAACNGAYTG 240
 Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 Db 241 GCNTYTMGNGTNGTNGTNGTNCAYTNGCNGTNCAYGCGNCAYTGGCGCARGCCNGAR 300
 Qy 101 GluAlaGlySerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
 Db 301 GARGCNGNAARWSNGAYWSNGARYTNCARGARWSMNGNAAYCCNNSNTYTCARGCNCAR 360
 Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
 Db 361 GTNGTNTYWSNTTYCARGCNTAYCCNATHGCMGNTGYGCNTYNTNGTNGTNCARGTN 420
 Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 Db 421 CCNGCNGAYTNTGTCARCCNGCNCARWSNGTNGGWSNCGTNTTYTAYTGYTGYTGYAR 480
 Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
 Db 481 GCNWSNTYTGNGCNGCARGTNCARATHTGGWSNTAYACNAARCCNMGNTAYCARAARGAR 540
 Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAspAsnValLeuLeuThr 196
 Db 541 YTNAAAYTNACNACARCARYTNCNGAYTGYMGNGGNTYNGARTNMGNGAYWSNATHCAR 600
 Qy 189 -----WSNTGYTGCGTNTYNTCCNGTNTAAAYGTNWSNACNGAYGCGGAYAAAYGTNTYNTNACN 660
 Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
 Db 661 YTNNGAYTGTWSNGARGARCARGAYTYSNTTYYTNTTAYTNTYTMGNCNGTNCNGAY 720
 Qy 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuLeuGlyProGlnAsnIleThrLeuAsnHis 236
 Db 721 GCNTYTNAAARWSNTYNTGGTAYAAARAAAYTNACNCGCNCARAAAYATHACNTYNTAAAYCAY 780
 Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
 Db 781 ACNGAYTNTGTCNCCNTGYTNTGYATHCARGTNTGWSNTYTCARCCNGAYWSNGARMGN 840
 Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
 Db 841 GTNGARTTYTGYCCTNTYTMGNGARGAYCCNGGNGCNCAYMGNAAAYTNTGGCAYATHGCN 900
 Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysLeuProGly 296

Db	1981	MGNTGARMGNGTGNACGCGCTTNGWNSGNTGAYWNTGVCNWSNWSN	2040
Qy	657	GlulAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu	674
Db	2041	GARGCNCNGTGTGTGARGARTGGGAYTTNGGNCCTGACNACNTTNGAR	2094
RESULT 11			
AA18133			
ID	AA18133	standard; cDNA; 2094 BP.	
XX	AA18133;		
XX	26-MAR-2002	(first entry)	
DT		Mouse DCRS7 reverse translation generic cDNA.	
DE		Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;	
XX		gene therapy; protein therapy; immunological disorder.	
XX		Mus musculus.	
XX	WO200190358-A2.		
XX	29-NOV-2001.		
XX	23-MAY-2001;	2001NO-US016767.	
XX	24-MAY-2000;	2000US-0206862P.	
XX	(SCHE)	SCHERING CORP.	
XX	Gorman DM;		
XX	WPI;	2002-106198/14.	
XX		Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide	
XX		useful for detecting antibodies generated in response to presence of	
XX		increased protein levels or immunological disorders.	
XX		Disclosure; Page 20-21; 148pp; English.	
XX		The invention relates to primate and rodent DNAX cytokine receptor	
XX		subunit (DCRS) polypeptides and the polynucleotides encoding them. The	
XX		receptors, or their portions may be useful as phosphate labelling enzymes	
XX		to label general or specific substrates. The subunits may also be	
XX		functional immunogens to elicit recognising antibodies, or antigens	
XX		capable of binding antibodies. A combination, e.g., including a DCRS can	
XX		be used as an immunogen for the production of antisera or antibodies	
XX		capable of distinguishing between other cytokine receptor family members.	
XX		A purified DCRS can also be used as a reagent to detect antibodies	
XX		generated in response to the presence of elevated levels of expression,	
XX		or immunological disorders which lead to antibody production to the	
XX		endogenous receptor. This sequence represents mouse DCRS7 reverse	
XX		translation generic cDNA	
XX	Sequence	2094 BP; 247 A; 251 C; 393 G; 285 T; 0 U; 918 Other;	
Alignment Scores:			
Pred. No.:	7.25e-183	Length:	2094
Score:	2637.00	Matches:	483
Percent Similarity:	69.2%	Conservative:	0
Best Local Similarity:	69.2%	Mismatches:	191
Query Match:	73.1%	Indels:	24
DB:	6	Gaps:	1
US-10-719-202-2 (1-674) x AA18133 (1-2094)			
Qy	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
Db	1	ATGCCGTWNSNTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	60
Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40

Db 61 YTNAGRMGNTNATGGARCCNARGAYACNGCMNGNTGYWSNTYNGGNTYTNWSNTGYCAY 120
Qy 41 LeuTriPAspGlyAapValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTNWGGGAYGGNGAYGTNTYNTGYTNCNGGWSNTYTCARWSNGCNCNGGNCNGTN 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTNGTNCNACNMGNNTNACACNGARGTYTNGTNTYTNMGNTGYCCNCARAAACNGAYTG 240
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTTPAlaGluProGlu 100
Db 241 GCNTYNTGYTNGMGNTGTNGTNCAYTNGCNGTNCAYGNCAYTGGCGNARGCCNGAR 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCNGNARWSNGAYWSNGARYTNCARGARWSNGNARAYGCNWSNTYTCARGCCNAR 360
Qy 121 ValValLeuSerPheGlnAlaTyProIleAlaArgCysAlaLeuLeuValGlnVal 140
Db 361 GTNGTNTYTNWSNTTYCARGCNTAYCCNATHGCMNGTGYGCNTYNTYNGARGTNCARGTN 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCNCGNGAYTNGTNCARCCNCGNCARWSNGTNGGWSNCGTNTTYGAYTYGYTYGAR 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTyrSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNTYNGCNGCNGARGTNCARATHGTGWSYATACNARCCNMGNTAYCARAARGAR 540
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 541 YTNAAAYTNACNARCARYTNCNGAYTYGWMGNGNTYTCARGTNGMNGAYWSNATHCAR 600
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 601 WSNTGYTGGTNTYTCNTGGYTNAAYTYTNWSNACNGAYGGNGAYAYGTNTYTNACN 660
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 661 YTNGAIGTWSNGARGARCARGAYTYTWSNTTYTNTYNTAYTNGMNCNGTNCNGAY 720
Qy 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 721 GCNTYTNARWSNTYNTGGTAYAAARAYTYTACNCGNCCNARAAAYATHACNTYTNAYCAY 780
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTyrSerLeuGluProAspSerGluArg 256
Db 781 ACNGAYTNGTNCNTGYTNTGYATHCARGTNTGGWSNTYTCARGCCNGAYWSNGARMGN 840
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTyrHisIleAla 276
Db 841 GTNGARTTYGYCCNTTYMGNGARGAYCCNGGNCNCAYMGNAAYTYTNGCAYATHGNCN 900
Qy 277 ArgLeuArgValLeuSerProGlyValTyrGlnLeuAspAlaProCysCysLeuProGly 296
Db 901 MGNNTYMGNTYTNWSNCCNGGNTGTGCGARYTNGAYGCNCCNTGYTYTNCNGCN 960
Qy 297 LysValThrLeuCysTyrGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 961 AARGTNCNTYNTGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNTYNTGTNCNCCN 1020
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1021 GTNCCNARAAAYGCNACNGTNAAYGARGCCNARGAYTYTCARYTNGTNGCNGNCAY 1080
Qy 337 ProAsnLeuCysValGlnValSerThrTyrGluLysValGlnLeuGlnAlaCysSerTyr 356
Db 1081 CCNAAAYTNTGYTNCARGTWSNACNTGGGARAARGTNCARYTNCARGCNTGYTNTGG 1140
Qy 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeu 376
Db 1141 GCNAYWSNTYNGCNCNTTYAARGAYGAYATGYTNTYNTGTNGARATGAARACNGGNTN 1200

Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1201 AAYAAVACNWSNGTNTGYCNYTNGARCCNWSNGNTGYACNCCNTYTNCCNWSNATGCGN 1260
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1261 WSNACNMGNGCNCNMGNTYTNNGGNGARGARYTNTYTCARGAYTYTMGNWSNCAYCARTGY 1320
Qy 417 MetGlnLeuTyrAsnAspAspAsnMetGlySerLeuTyrAlaCysProMetAspLysTyr 436
Db 1321 ATCCARYTNTGGAYGAYGAYATGGGWSNTYTNWGGCNGTGYCCNATGGAYAAATAY 1380
Qy 437 IleHisArgArgTyrValLeuValTyrLeuAlaCysLeuLeuAlaAlaLeuPhe 456
Db 1381 ATHCAYMGNGMTGGTNTYNTGTNGTNGCNYTNTYTNWTCNCGCNGCNYTNTTY 1440
Qy 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1441 TTYTYYTNTYNTNAAARAARGAYTMGNMGNAARGCNGCMNGGWSNMGNACNCGCNYTN 1500
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1501 YTNNTYTCAYWSNGCNGAYGGGCGNGNTAYGARMGNTYTNGTNGGNGCNYTNCGNWSNGCN 1560
Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTyrSerArgArgGluLeuSerAla 516
Db 1561 YTNWSNARATGCCNTYTNMGNTGCGTNGAYTYTNGWSNMGNMGNGARYTNWSNGCN 1620
Qy 517 HisGlyAlaLeuAlaTyrPheHisHisGlnArgArgIleLeuGlnGluGlyVal 536
Db 1621 CAYGGNGCNYTNGCNYTGGTTCAYCAYCARMGWSNMGNAATHYTNARGARGGNGGNTN 1680
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTyrLeuGlnLeuGln 556
Db 1681 GTNATHYNTYNTYTNWSNCCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCAR 1740
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTyrLeuSerCysValLeuProAsp 576
Db 1741 ACNGTNGARCCNGCNCNCAAYGAYGCNTYTCNCGCNGTGGYTWSNTGYGTNTYTNCCNGAY 1800
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTYTTCARGGNGMNGCNCNCGMGTAYGTNGGNGTNTAYTYTGAYGGNTYNTNCAY 1860
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCNGAYWSNGTNCNWSNCCNTTYMGNTGNGCNCNTYTNWNTYTNCCNWSNCARYTN 1920
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCNCGCNTYTYTNGAYGCNTYTCARGGNGGNTGYWSNACNWSNCGNMGNCNCGNGAY 1980
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 1981 MGNGTNGARMGNTNACNARGCNYTNMGWSNCGNYTNGAYWSNTGYACNWSNWSN 2040
Qy 657 GluAlaProGlyCysCysGluGluTyrAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GARGCNCNGGNTGYTGYGARGARTGGGAYTYTNGGNCNTGYACNACNCTYTNGAR 2094

RESULT 12

AAC85027
ID AAC85027 standard; cDNA; 2255 BP.

XX AAC85027;

XX 08-MAY-2001 (first entry)

DE Human cytokine receptor Zcytor14 encoding cDNA.

XX Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine; ss.
KW

101	Glu	-----AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer	116
102	Asp		117
103	Asp		118
104	Asp		119
105	Asp		120
106	Asp		121
107	Asp		122
108	Asp		123
109	Asp		124
110	Asp		125
111	Asp		126
112	Asp		127
113	Asp		128
114	Asp		129
115	Asp		130
116	Asp		131
117	Asp		132
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205	Asp		220
206	Asp		221
207	Asp		222
208	Asp		223
209	Asp		224
210	Asp		225
211	Asp		226
212	Asp		227
213	Asp		228

Db 574 GAGGTGCAAGTGCCTGCTGCGCCCTTGTGCGAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT 633
Qy 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArg 176
Db 634 GACTGCTTCAGGGCTGCGCTAGGAGTGGAGTACGAATCTGGTCTATACTCAGCCCGAGG 693
Qy 177 TyrGlnLysGluLeuAenLeuThrGlnGlnLeuPro----- 188
Db 694 TACGAGAAGGAACCTCAACACACACAGCAGCTGCTGCGCTCGCTCAACGTGTCA 753
Qy 189 ---AspGlyAspAenValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe 207
Db 754 GCAGATGGTGAACAGTGCATCTGGTCTGTAATGTCTCTGAGGAGCAGCACTTCGGCCTC 813
Qy 208 LeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTyrLysAenLeuThr 227
Db 814 TCCCTGTACTGAATCAGTTCAGGGCCCGCCCAAAACCCCGGTGGCACAAAACCTGACT 873
Qy 228 GlyProGlnAenIleThrLeuAenHisThrAspLeuValProCysLeuCysIleGlnVal 247
Db 874 GGACCGCAGATCATTTACCTTGAACCCACACAGACCTGGTTCCTGCTCTGTATTACAGGTG 933
Qy 248 TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly 267
Db 934 TGGCTCTTGGAACTTGAATCTCGTTAGGAGCAATCTGCTCCCTTCAGGAGAGACCCCGC 993
Qy 268 AlaHisArgAenLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287
Db 994 GCACACAGAACCTCTGCAAGCGCCGAGTGCAGTCTGACCTGCACCTGCAGAGCTGGCTG 1053
Qy 288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln 307
Db 1054 CTGGACGACCGCTGCTGCTGCGCCCGCAAGCGGCACCTGTGCTGGCGGGCTCCGGGTGGG 1113
Qy 308 SerProCysGlnProLeuValProValProGlnLysAenAlaThrValAenGluPro 327
Db 1114 GACCCCTGCCAGCACTGGTCCACCGCTTCTCTGGGAGACGTCACCTGTGACAAAGGTT 1173
Qy 328 GlnAspPheGlnLeuValAlaGlyHisProAenLeuCysValGlnValSerThrTrpGlu 347
Db 1174 CTCGAGTTCCCATCTGTAAGGCCACCTACCTCTGTGTTTCAAGTGAACAGCTTCGGAG 1233
Qy 348 LysValGlnLeuAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet 367
Db 1234 AAGCTGCAGCTCAGAGAGTCTGTGGGTGACTCCCTGGGGCCCTCAAGACAGATGG 1293
Qy 368 LeuLeuValGluMetLysThrGlyLeuAenThrSerValCysAlaLeuGluProSer 387
Db 1294 CTACTGTTGGACACAGAGGCCCGCCAGGACAAACAGATCCCTCTGTGCTTGGAACTCAGT 1353
Qy 388 GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu 407
Db 1354 GGCTGTACTTCACTACCCAGCAAGCCTCCACGAGGCGAGCTCGCTTGGAGAGTACTTGA 1413
Qy 408 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAlaAspAsnMetGlySer 427
Db 1414 CTACAGACCTCGCAGTCAGCCAGTGTCTGCAGCTATAGG---GACGATGACTGGGAGCG 1470
Qy 428 LeuTrpAlaCysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAla 447
Db 1471 CTATGGCCCTGCCCATGACAAATATATCCACAGCGCTGGGCCCTCTGTGTGGTGGCC 1530
Qy 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys 467
Db 1531 TGCCTACTCTTTGGCCGCTCGCTTTCCTCATCTCTCTCTCAAAAGGATCAGCGGAAA 1590
Qy 468 AlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu 487
Db 1591 GCGCGCCGACGGGGCGCGGCTCTGCTCTCTACTCAGCCGATGACTCGGGTTTCGAG 1650
Qy 488 ArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAsp 507
Db 1651 CGCCTGGTGGGGCCCTGGCGCTCGGCCCTGTGTCAGCTCGCGCTGGCGCTAGAC 1710

Qy 508 LeuTrpSerArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArg 527
Db 1711 CTGTGGAGCGTCTGTAACTAGAGCCGCACAGGGCCCGCTTGGTTTTCACCCGACGGG 1770
Qy 528 ArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerProAlaAlaValAla 547
Db 1771 CGCAGACCTTCAGAGAGGGCGGTGTGTCTTCTCTCTCCCGGTGGTGGCG 1830
Qy 548 GlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro-----GlyProHisasp 564
Db 1831 CTGTGCAGCAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGCGCACCGCCCGAC 1890
Qy 565 AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly 584
Db 1891 GCCTTCGCGGCTCGCTCAGCTGCTGCTGCTGCCGACCTTCTTGCAGGGCGGGCGCCCGC 1950
Qy 585 ArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPhe 604
Db 1951 AGCTACGTGGGGCTGCTTCGACAGCTGTCTCCACCGGACGCGTACCGCCGCTTTTC 2010
Qy 605 ArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGln 624
Db 2011 CGCACCGTGGCGTCTTACACTGCTCCCTCCCACTGCCAGACTTCTCTGGGGGCCCTGCG 2070
Qy 625 GlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla 644
Db 2071 CAGCTCGCGCCCGCTTCGGGGCGGCTCCAAAGAGAGCGGAGCAAGTGTCCCGGGCC 2130
Qy 645 LeuArgSerAlaLeuAspSerCys-----ThrSerSerSerGluAlaProGly 660
Db 2131 CTTTCAGCGACGCTTGGATAGTACTTCCATCCCGGGGACTCCCGCGCGGGA 2184
RESULT 14
AEF05348
ID AEF05348 standard; cDNA; 2255 BP.
XX
AC AEF05348;
XX 23-FEB-2006 (first entry)
XX
DE Human IL17A and F receptor zcytoR14 cDNA SEQ ID NO 1.
XX
KW antiinflammatory; antiaesthetic; gastrointestinal-gen.; antiulcer;
KW antiarthritic; dermatologic; antipsoriatic; antibacterial;
KW immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
KW inflammatory bowel disease; asthma; respiratory disease;
KW ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;
KW gastroenteral disease; psoriasis; antipsoriatic;
KW musculoskeletal disease; immune disorder; atopic dermatitis;
KW dermatological disease; endotoxemia; inflammation; endotoxic shock; sepsis;
KW dermatological; immunosuppressive; infection; zcytoR14; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154..2232
FT /tag= a
FT /product= "zcytoR14x1"
FT 214..1509
FT /tag= b
FT /product= "zcytoR14x1"
FT /partial
FT /note= "No start or stop codon given"
XX
PN WO2005123778-A2.
XX
XX
PD 29-DEC-2005.
XX
XX 10-JUN-2005; 2005WO-US020521.
XX
XX 10-JUN-2004; 2004US-0578805P.
PR

XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
 PI Jaspers SR, Billeborough J;
 XX WPI; 2006-067457/07.
 DR P-PSDB; AEF05349, AEF05350.
 DR
 XX New isolated soluble receptor comprises at least one Zcytor14 subunit,
 PT useful for treating an inflammatory disease, e.g. asthma, inflammatory
 PT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
 PT psoriasis.
 XX
 XX Example 28; SEQ ID NO 1; 205pp; English.
 XX
 CC The invention describes an isolated soluble receptor comprises at least
 CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
 CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
 CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
 CC ID NO. 24) given in the specification. Also described are: an isolated
 CC soluble receptor comprising zcytor14, where Zcytor14 comprises a
 CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
 CC the pro-inflammatory activity of either IL-17A comprising fully defined
 CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
 CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
 CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
 CC and where the antibody or antibody fragment reduces the pro-inflammatory
 CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
 CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
 CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
 CC role; and treating a pathological condition in a subject associated with
 CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
 CC subunit is useful for treating an inflammatory disease, e.g. asthma;
 CC chronic inflammatory disease selected from inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
 CC psoriasis; or acute inflammatory disease selected from endotoxemia,
 CC septicemia, toxic shock syndrome, or infectious disease. This sequence
 CC represents human IL-17A and IL-17F receptor zcytor14.
 XX
 SQ Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,88e-162 Length: 2255
 Score: 2352.50 Matches: 457
 Percent Similarity: 77.1% Conservative: 66
 Best Local Similarity: 67.4% Mismatches: 136
 Query Match: 65.3% Indels: 19
 DB: 15 Gaps: 5

US-10-719-202-2 (1-674) x AEF05348 (1-2255)

QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
 DB 154 ATGCGTGTGCCCTGGTTCCTGTGCTTGGCACTGGGCCGGAAGCCAGTGCCTTTCT 213
 QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 DB 214 CTGGAGAGCTTGTGGGGCTCAGGACGCTACCCACTGCTCTCCGGGCTCTCTTGGCCGC 273
 QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 DB 274 CTCTGGGACAGTGACATCTCTGCTGCTGGGGACATGCTGCTCCGGGCTCTCTTGGCCGC 333
 QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 DB 334 CTGGGCGCTTACGCACCTCGCAGACAGAGCTGGTGGCTGAGGTGCGCAGAGGAGCACCAGTCT 393
 QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 DB 394 GACCTCTGTCTGGGTGGCTGTCCACTTGGCCGCTGATGGGCACCTGGGAGAGGCTGAA 453
 QY 101 Glu-----AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 116

DB 454 GATGAGGAAAAGCTTTTGGAGGACGAGCTGACTCAGGGGTGGAGGAGCTTAGGAATGCCTCT 513
 QY 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyProIleAlaArgCysAlaLeuLeu 136
 DB 514 CTCAGAGCCCAAGTCGTCTCTCTCCAGGCTACCTTCTGAGGAGGAGCTTGGCTGCTGCTG 573
 QY 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156
 DB 574 GAGGTGCAAGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
 QY 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyTrpLysProArg 176
 DB 634 GACTGCTTCGAGGCTGCCCTAGGAGTACGAGTACGAATCTGCTCTATCTACTCAGCCAGG 693
 QY 177 TyrGlnLysGluLeuAsnLeuThrGlnLeuPro----- 188
 DB 694 TAGGAGGAGAACTCAACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
 QY 189 ---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPhe 207
 DB 754 GCAGATGGTGACACAGTGCATCTGGTTCCTGAATGCTCTGAGGAGCAGCAGCTTGGCCCTC 813
 QY 208 LeuLeuTyTrpLeuArgProValProAspAlaLeuLysSerLeuTrpTyTrpLysAsnLeuThr 227
 DB 814 TCCCTGTACTGGAATCAGGTCCAGGCGCCGCCCAAAACCCCGGTGGCAGCAAAAACCTGACT 873
 QY 228 GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysValleGlnVal 247
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 QY 268 AlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287
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 QY 408 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspMetGlySer 427
 DB 1414 CTACAAGACCTGCAGTCAGGCCAGTGTCTGACGCTATGG---GACGATGTTGGAGCG 1470
 QY 428 LeuTrpAlaCysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAla 447
 DB 1471 CTATGGGCTGCGCCCATGACAAATACATCCACAGCGCTGGGCCCTCTGTTGGCTGGCC 1530
 QY 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys 467

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Db      1531  TGCCTACTCTTTGGCGCTGGCGCTTTCCTCATCTCTCTCTCAAAAAGGATCAGCGGAAA 1590
Qy      468  AlalaArgGlySerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu 487
Db      1591  GCGCGCGCAGGCGCGCGCGCTCTGCTCTCTACTCAGCGGATGACTCGGGTTTCGAG 1650
Qy      488  ArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAsp 507
Db      1651  GCGCTGGTGGCGCGCTGGCGCTGTGCCAGCTGCGCTGCGCGTGGCGCGTAGAC 1710
Qy      508  LeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArg 527
Db      1711  CTGTGGAGCCGTGCTGAACAGCGCGCAGGCGCGCGTGGCTTGGTTTTCACGCCGAGCGG 1770
Qy      528  ArgArgLeuGlnGlnGlyValValValLeuLeuPheSerProAlaAlaValAla 547
Db      1771  CGCCAGACCTTCAGAGGCGCGCGTGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1830
Qy      548  GlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro-----GlyProHisAsp 564
Db      1831  CTGTGACGAGTGGCTACAGGATGGGTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGC 1890
Qy      565  AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly 584
Db      1891  GCCTTCCGCGCTCGCTTCAGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1950
Qy      585  ArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPhe 604
Db      1951  AGCTACGTGGGCGCTGCTTCAGAGGCTGTCTCCACCGCGAGCGCGCTACCGCGCTTTC 2010
Qy      605  ArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGln 624
Db      2011  CGCACCGTGGCGCTTTCACACTGCTCCCTCCCACTGCCAGACTTCTGGGGGCGCTGCAG 2070
Qy      625  GlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla 644
Db      2071  CAGCTTCGCGCGCGCTTCGCGCGCTCCCAAGAGAGAGCGGAGCAAGTGTCCCGGCGC 2130
Qy      645  LeuArgSerAlaLeuAspSerCys-----ThrSerSerSerGluAlaProGly 660
Db      2131  CTTACGCCAGCGCTGGATGACTACTTCCATCCCGCGGAGCTCCCGCGCGCGGGA 2184

RESULT 15
ID      AAS46223 standard; cDNA; 2380 BP.
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AC      AAS46223;
DT
DE      Human DNA encoding PRO polypeptide sequence #299.
XX
XX      PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW      dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW      blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW      adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW      PCR primer.
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OS      Homo sapiens.
PN      WO200168848-A2.
XX
PD      20-SEP-2001.
XX
PF      28-FEB-2001; 2001WO-US0006520.
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PR      01-MAR-2000; 2000WO-US0005601.
PR      02-MAR-2000; 2000WO-US0005841.
PR      03-MAR-2000; 2000US-0187202P.
PR      06-MAR-2000; 2000US-0186968P.
PR      14-MAR-2000; 2000US-0189320P.
PR      14-MAR-2000; 2000US-0189328P.
PR      15-MAR-2000; 2000WO-US0006884.
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PR      21-MAR-2000; 2000US-0190828P.
PR      21-MAR-2000; 2000US-0191007P.
PR      21-MAR-2000; 2000US-0191048P.
PR      21-MAR-2000; 2000US-0191314P.
PR      28-MAR-2000; 2000US-0192655P.
PR      29-MAR-2000; 2000US-0193032P.
PR      29-MAR-2000; 2000US-0193053P.
PR      30-MAR-2000; 2000WO-US0008439.
PR      04-APR-2000; 2000US-0194449P.
PR      04-APR-2000; 2000US-0194647P.
PR      11-APR-2000; 2000US-0195975P.
PR      11-APR-2000; 2000US-0196000P.
PR      11-APR-2000; 2000US-0196187P.
PR      11-APR-2000; 2000US-0196690P.
PR      11-APR-2000; 2000US-0196820P.
PR      18-APR-2000; 2000US-0198121P.
PR      18-APR-2000; 2000US-0198585P.
PR      18-APR-2000; 2000US-0199397P.
PR      25-APR-2000; 2000US-0199550P.
PR      25-APR-2000; 2000US-0199654P.
PR      03-MAY-2000; 2000US-0201516P.
PR      17-MAY-2000; 2000WO-US013705.
PR      22-MAY-2000; 2000WO-US014042.
PR      30-MAY-2000; 2000WO-US014941.
PR      02-JUN-2000; 2000WO-US015264.
PR      05-JUN-2000; 2000US-0209832P.
PR      28-JUN-2000; 2000WO-US020710.
PR      22-AUG-2000; 2000US-00644848.
PR      24-AUG-2000; 2000WO-US023328.
PR      08-NOV-2000; 2000WO-US030952.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000WO-US034956.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PU, Gurney AL;
PI      Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX      WPI; 2001-602746/68.
XX      P-PSDB; AAU29322.
XX
XX      Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT      presence of tumors, such as prostate and breast tumors, in mammals and to
PT      screen for modulators of the compounds.
XX
XX      Claim 2; Fig 597; 774pp; English.
XX
XX      Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC      primers for PRO polypeptides of the invention. The sequences of the
CC      invention can be used to detect the presence of a tumour in a mammal by
CC      comparing the level of expression of a PRO polypeptide in a test sample
CC      of cells from the animal and a control sample of normal cells, whereby a
CC      higher level of expression in the test sample indicates the presence of a
CC      tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC      pigs, goats and rabbits but are preferably human. The polypeptides can be
CC      used to stimulate tumour necrosis factor (TNF) alpha release from human
CC      blood, when contacted with it. A specific polypeptide can be used to
CC      stimulate the proliferation or differentiation of chondrocyte cells. The
CC      PRO proteins can be used to determine the presence of tumours and also
CC      susceptibility to tumour development, particularly adrenal, lung, colon,
CC      breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC      subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC      can be used for genetic analysis of individuals with genetic disorders
XX
XX      Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 5,07e-161 Length: 2380
Score: 2339.00 Matches: 459
Percent Similarity: 75.3% Conservative: 66
Best Local Similarity: 66.3% Mismatches: 133
Query Match: 64.9% Indels: 34
DB: 4 Gaps: 7
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us-10-719-202-2.p2n.rng

Tue Aug 22 11:34:35 2006

GenCore version 5.1.1.9
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OM protein - nucleic search, using frame_plus_p2n_model

Run on: August 17, 2006, 08:41:10 ; Search time 8893 Seconds
(without alignments)
7278.042 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605
Sequence: 1 MPVSWFLSLALGRNPVVVS.....SSEAPGCCCEWDLGCTTLE 674

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB_spool/US10719202/runat_16082006_095631_13229/app_query.fasta_1
-DB=GenEmbl -QMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05p
-USER=US10719202 @CNG 1.1 8328 @runat_16082006_095631_13229 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_scs:*
8: gb_sy:*
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10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_cm:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	2153	6 AF458066	AF458066 Mus muscu
2	3605	100.0	2256	2 AX360307	AX360307 Sequence
3	3583	99.4	2328	2 AX360310	AX360310 Sequence

4	3572.5	99.1	2269	2	CS251263	CS251263 Sequence
5	3569.5	99.0	2287	2	CS251267	CS251267 Sequence
6	3565	98.9	2314	2	CS135270	CS135270 Sequence
7	3565	98.9	2314	2	AX350976	AX350976 Sequence
8	3539	98.2	2331	2	AX720728	AX720728 Sequence
9	2995.5	83.1	2015	6	BC004759	BC004759 Mus muscu
10	2866	74.0	2022	2	AX360309	AX360309 Sequence
11	2644	73.3	2094	2	AX360312	AX360312 Sequence
12	2637	73.1	2094	2	AX350978	AX350978 Sequence
13	2352.5	65.3	2255	2	CS251239	CS251239 Sequence
14	2352.5	65.3	2255	2	AX073993	AX073993 Sequence
15	2339	64.9	2380	2	CS255725	CS255725 Sequence
16	2339	64.9	2380	2	CS257646	CS257646 Sequence
17	2339	64.9	2380	2	CS257816	CS257816 Sequence
18	2339	64.9	2380	2	CS257986	CS257986 Sequence
19	2339	64.9	2380	2	AR338362	AR338362 Sequence
20	2339	64.9	2380	2	AX092430	AX092430 Sequence
21	2339	64.9	2380	2	AX180776	AX180776 Sequence
22	2339	64.9	2380	2	AX376530	AX376530 Sequence
23	2339	64.9	2380	2	AX454778	AX454778 Sequence
24	2339	64.9	2380	2	AX491256	AX491256 Sequence
25	2339	64.9	2380	5	AV359098	AV359098 Homo sapi
26	2335	64.8	2350	2	AX720680	AX720680 Sequence
27	2332	64.7	2369	5	AY358840	AY358840 Homo sapi
28	2325.5	64.5	2395	5	AF458065	AF458065 Homo sapi
29	2320.5	64.4	2402	2	AX720682	AX720682 Sequence
30	2316.5	64.3	2507	5	BC006411	BC006411 Homo sapi
31	2316.5	64.3	2527	2	CQ899436	CQ899436 Sequence
32	2306.5	64.0	2163	2	AX720657	AX720657 Sequence
33	2306.5	64.0	2344	2	AX720659	AX720659 Sequence
34	2305	63.9	2497	2	AX720672	AX720672 Sequence
35	2294.5	63.6	2698	2	DD178425	DD178425 SECRETED
36	2281	63.3	2622	2	AR718826	AR718826 Sequence
37	2281	63.3	2622	2	AX747801	AX747801 Sequence
38	2281	63.3	2622	5	AK092907	AK092907 Homo sapi
39	2269	62.9	2180	2	CS251261	CS251261 Sequence
40	2235	62.0	2308	2	CS135268	CS135268 Sequence
41	2235	62.0	2308	2	AX350973	AX350973 Sequence
42	2222	61.6	2343	2	AX720678	AX720678 Sequence
43	2184	60.6	2314	2	AX720676	AX720676 Sequence
44	2182	60.5	2499	2	BD123623	BD123623 Secretary
45	2182	60.5	2499	2	CS051377	CS051377 Sequence

ALIGNMENTS

RESULT 1	AF458066	Mus musculus IL-17RC mRNA, complete cds.	2153 bp	mRNA	linear	ROD 15-JUL-2002
LOCUS	AF458066					
DEFINITION	AF458066					
ACCESSION	AF458066.1	GI:21779859				
VERSION						
KEYWORDS						
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;					
	Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 2153)					
AUTHORS	Gilbert, J.M. and Gorman, D.M.					
TITLE	Identification of novel IL-17 related receptors					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 2153)					
AUTHORS	Gilbert, J.M. and Gorman, D.M.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901					
	California Ave., Palo Alto, CA 94304, USA					
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CDS						

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ORIGIN

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Score: 3605.00 Matches: 674
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-719-202-2 (1-674) x AF458066 (1-2153)

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DB 110 ATGCCTGTGTCTGCTGCTGTCTGTGGACCTGGGCGGAAACCTGTGTGTCTCTCT 169
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 170 CTGGAGAGACTGATGAGGCTCAGACACTGACCGCTGTCTCTAGGCTCTCTCTGCCAC 229
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 230 CTCTGGGATGGTGTGCTGTCTGCTGTGGCTGTGAGGCTCCAGTCTGCCCGGCGCTGTG 289
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
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DB 350 GCCCTCCGTGTCCGT 409
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
DB 410 GAAGCTGGAAGTCTGATTCAAGACTCCAGGAGTCTAGGAACGCTCTCTCCAGGCGCCAG 469
QY 121 ValValLeuSerPheGlnAlaValProLeuAlaArgCysAlaLeuLeuGluValGlnVal 140
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QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 530 CCCGCTGACCTGGTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
QY 161 AlaSerLeuGlyAlaGluValGlnLysTrpSerGlyThrLysProArgGlyTrpGlnLysGlu 180
DB 590 GCTAGTCTTGGGCTGAGGTACAGATCTGCTTACACGAGCCAGGCTACCAAGAAAGAG 649
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QY 201 GluGlnGlnAspPheSerPheLeuLeuTrpLeuArgProValProAspAlaLeuLysSer 220
DB 710 GAGGAGCAGGACTTAGTCTTCTTACTGTACCTGTGCTCCAGTCCCGGATGCTCTCAATCC 769

QY 221 LeuTrpTrpLysAsnLeuThrGlyProGlnAsnLysLeuAsnHisThrAspLeuVal 240
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QY 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
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QY 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
DB 1310 GCTGCTGCTGGGAGAGAGT 1369
QY 421 AsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg 440
DB 1370 AACGATGACACATCGGATCGTATGGGCTGTCCCTCCACAGTACATCCACAGCGCG 1429
QY 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
DB 1430 TGGGTCTTAGTATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTT 1489
QY 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
DB 1490 CTAAAAAAGGACCGCAGGAAAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1549
QY 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
DB 1550 GCCGACGAGCGGGCTACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1609
QY 501 ProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
DB 1610 CCACCTGCGCTGGCGTGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1669
QY 521 AlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeuLeu 540
DB 1670 GCTGTGTTCACACACAGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1729
QY 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
DB 1730 TTCTGTCCCGCGCGCTGT 1789
QY 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
DB 1790 GGGCGCATGACGCTGT 1849
QY 581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600

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Db      1850 CCGGGACCGCGCGTCTACTTCGAGCGGCTGCTGCACCGACTCTGTG 1909
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Db      1910 CCTCCCGGTTCGGCGTCCGCCGCTCTCTCCCTGCCACGACGCTGCCGGCTTCCTG 1969
Qy      621 AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
Db      1970 GATGCACTGACGGAGGCTGCTCCACTTCGGGGGCGACCGCGGACCGGGTGAACGA 2029
Qy      641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
Db      2030 GTGACCCAGCGCTGCGGTCGCGCTTGGACAGCTGTACTTCTAGTCTCGGAAGCCCCAGGC 2089
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Db      2090 TGCTCGGAGGATGGACCTGGGACCTGCACCTACACTAGAA 2131

RESULT 2
AX360307
LOCUS      AX360307                2256 bp    DNA        linear    PAT 13-FEB-2002
DEFINITION Sequence 1 from Patent WO0204519.
ACCESSION  AX360307
VERSION     AX360307.1  GI:18675809
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS   Gao, Z.
TITLES    Murine cytokine receptor
JOURNAL   Patent: WO 0204519-A.1 17-JAN-2002;
           Zymogenetics, Inc. (US)
FEATURES   Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      0      Length:      2256
Score:          3605.00  Matches:      674
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match:      100.0%  Indels:      0
DB:              2      Gaps:        0

US-10-719-202-2 (1-674) x AX360307 (1-2256)

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Qy	401	AlaArgLeuGlyGluGluLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp	420
Db	1397	GCTCGCCTGGGAGAGAGATTGCTGCAGACTTCCGATCACACAGTGTATGAGCTGTGG	1456
Qy	421	AsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg	440
Db	1457	AACGATGACAAATGGGATCGTATGGCGCTGCCCATGGACAGTACATCACAGGGCG	1516
Qy	441	TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu	460
Db	1517	TGGGTCTTAGTATGGCTGGCTGCTCTTGGCTGGCGGCTTTCTTCTTCCTCTCT	1576
Qy	461	LeuLysLysAspArgAlaAlaAlaAlaArgGlySerArgThrAlaLeuLeuHisSer	480
Db	1577	CTAAATAAGGACCGCAGAGAGCGCGTGGCTCCCGCAGCGCTTGTCTCCACTCC	1636
Qy	481	AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet	500
Db	1637	GCCGACGAGCGGGCTACGAGCGTCTGGTGGAGCACTGGCGTCCGCTTGAGCCAGATG	1696
Qy	501	ProLeuArgValAlaValaAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeu	520
Db	1697	CCACTGCGCGTGGCGTGGACCTGTGGAGCGCGCGAGCTGAGCGCGACGAGCCCTA	1756
Qy	521	AlaTrpPheHisGlnArgArgIleLeuGlnGluGlyValValValIleLeuLeu	540
Db	1757	GCCTGTTTCCACCACGAGCGCGTATCTCTGAGAGGGTGGGTGTAATCTTCTC	1816
Qy	541	PheSerProAlaAlaValaGlnCysGlnInTrpLeuGlnLeuGlnThrValGluPro	560
Db	1817	TTCTCGCGCGCGCGTGGCGAGTGTACGAGTGGCTGCGAGTCCAGACAGTGGAGGCC	1876
Qy	561	GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly	580
Db	1877	GGCGCGCATGACGCGCTCGCGCGCTGGCTCAGCTCGTGTACCCGATTTCTGCAAGCC	1936
Qy	581	ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal	600
Db	1937	CGGGGACCGCGCTACGTGGGGTCTACTTCGAGCGGCTGTCACCCAGCTCTGTG	1996
Qy	601	ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu	620
Db	1997	CCCTCCCGCTTCCGGGTGCGCCCGCTTCTCTCCCTGCCACAGCAGTGGCGGCTTTCCTG	2056
Qy	621	AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg	640
Db	2057	GATGCACTGCAGGAGGCTGCTCCACTTCCGCGGGCGACCCCGGACCGGGTGGACGA	2116
Qy	641	ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerGluAlaProGly	660
Db	2117	GTGACCCAGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTAGCTCGGAGCCCGAGCC	2176
Qy	661	CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu	674
Db	2177	TGCTGCGAGGAATGGACCTGGGACCTGCACTACACTAGAA	2218
RESULT 3			
AX360310			
LOCUS	AX360310	2328 bp	DNA linear PAT 13-FEB-2002
DEFINITION	Sequence 4 from Patent WO0204519.		
ACCESSION	AX360310		
VERSION	AX360310.1	GI:18675812	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
. REFERENCE	1		

AUTHORS	Gao, Z.		
TITLE	Murine cytokine receptor		
JOURNAL	Patent: WO 0204519-A 4 17-JAN-2002;		
FEATURES	ZymoGenetics, Inc. (US)		
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Alignment Scores:			
Pred. No.:	0		
Score:	3583.00		
Percent Similarity:	96.6%		
Best Local Similarity:	96.6%		
Query Match:	99.4%		
DB:	2		
	Length: 2328		
	Matches: 674		
	Conservative: 0		
	Mismatches: 0		
	Indels: 24		
	Gaps: 1		
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Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	257	CTGGAGAGACTGATGAGCCTCAGGACCTGACCGCTGCTCTTAGGCTCTCTCTGCCAC	316
Qy	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	317	CTCTGGGATGGTACGCTGCTCTGCTGCTGGAAGCCTCCAGTCTGCCCGCCCTGTG	376
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
Db	377	CTAGTGCTTACCCGCTGCAGACGAGCTGGTGTGAGGTGCCACAGAGACAGATTGC	436
Qy	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
Db	437	GCCTCCGTGTCCTGTGGTGTCCACTTGGCCGTGATGGGACCTGGGCGAGCCTGAA	496
Qy	101	GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln	120
Db	497	GAAGCTGGAAGTCTGATTCAAACTCCAGGAGTCTAGGAACGCCTCTCTCCAGGCCAG	556
Qy	121	ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal	140
Db	557	GTGGTGCTCTCTTCCAGGCCTACCCCATCGCCCGCTGTGCCGTATTTGACGTGTTTCGAG	616
Qy	141	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
Db	617	CCCGCTGACCTGGTGACGCTGGTCACTCCGTGGGTTCGCGGTATTTGACTGTGTTTCGAG	676
Qy	161	AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu	180

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 Db 737 CTCACCTTCACACAGCAGCTGCTGACTGCGAGGGGTCTTGAAGTCCGGGACAGCATCCAG 796
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 Qy 377 AsnAenThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
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RESULT 4
 LOCUS CS251263 2269 bp DNA linear PAT 18-JAN-2006
 DEFINITION Sequence 25 from Patent WO2005123778.
 ACCESSION CS251263
 VERSION CS251263.1 GI:85361024
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Presnell, S.R.
 TITLE Soluble zcytor14, anti-zcytor14 antibodies and binding partners and methods of using in inflammation
 JOURNAL Patent: WO 2005123778-A 25 29-DEC-2005;
 ZymoGenetics, Inc. (US)

FEATURES
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 Score: 3572.50 Matches: 671
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 Best local Similarity: 98.2% Mismatches: 2
 Query Match: 99.1% Indels: 9
 DB: 2 Gaps: 1

US-10-719-202-2 (1-674) x CS251263 (1-2269)

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AX350976
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DEFINITION Sequence 10 from Patent WO0190358.
ACCESSION AX350976
VERSION AX350976.1 GI:18616352
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
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unclassified sequences.
1
REFERENCE
AUTHORS Gorman,D.M.
TITLE Mammalian receptor proteins: related reagents and methods
JOURNAL Patent: WO 0190358-A 10 29-NOV-2001;
FEATURES SCHERING CORPORATION (US)
Location/Qualifiers
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ORGANISM	Mus sp.		
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AUTHORS	Haudenschild, D., Rose, L., Moseley, T. and Reddi, A.H.		
TITLE	IL-17 receptor-like protein, uses thereof, and modulation of catabolic activity of IL-17 cytokines on bone and cartilage		
JOURNAL	Patent: WO 0238764-A 74 16-MAY-2002;		
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LOCUS
DEFINITION

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Tue Aug 22 11:34:34 2006

ACCESSION BC004759
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 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scaplenko, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tohiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, V.S., Kzyvinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Strausberg, R.
 Direct Submission
 Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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ORIGIN

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 Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
 Db 717 CTCAACTCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776

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189 QY -----AspGlyAspAenValLeuLeuThr 196
190 DB AGCTGCTGGGTCCTGCCCTCAATGCTGTCTACAGATGTCACATGTCCTTCTGACA 836
191 QY LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
192 DB CTGATGTCCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTGTCCAGTCCCGGAT 896
193 QY AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
194 DB GCTCTCAATCCTTGTGTGACAAAACCTGACTGGACCTCAGAACATTTACTTTAAACCAC 956
195 QY ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
196 DB ACAGACCTGGTTCCTGCTCCCTCTGCAATTCAGGTGTGTGCTAGAGCCAGAGCTCTGAGAGG 1016
197 QY ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
198 DB GTGCAATTCGTGCCCTTCCGGGAGATCCCGGTGCAACAGGAACCTCTGGCACATAGCC 1076
199 QY ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
200 DB AGCTGCGGTACTGTCCCGGGGTATGGCAGTATGGGCTTGTCTGTCTGCCGGC 1136
201 QY LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
202 DB AAGTAACTGTGTGCCAGGCACACAGAGTCCCTGCCAGCCACTTGTGCCACCA 1196
203 QY ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
204 DB GTGCCCCAGAGAACCGCATCTGTAATGGCCACAGATTTCCAGTTGGTGGCAGGCCAC 1256
205 QY ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
206 DB CCCAACCTCTGTCTCAGGTGAGCACCCTGGAGAGGTTGAGTGCAGAGGTCTGTGTGG 1316
207 QY AlaAspSerLeuGlyPropheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
208 DB GCTGACTCCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGAGATGAAACCGGGCTC 1376
209 QY AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
210 DB AACAAACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1436
211 QY SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
212 DB TCACGAGAGCTGCTCCCTGGGAGAGGTTGCTGCAAGATCTCCAGATCCACACCATGT 1496
213 QY MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
214 DB ATGCAGCTGTGGAACGATGACACATGGGATGCTATGGGCTGCCCATGGACAGTAC 1556
215 QY IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
216 DB ATCCACAGGCGCTGGTCTAGTATGGCTGCCCTGCTACTCTTGGTGGCGGCTTTTC 1616
217 QY PhePheLeuLeuLeuLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
218 DB TTCTTCTCTCTTCT-AAAAA----- 1636
219 QY LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
220 DB ----- 1636
221 QY LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla 516
222 DB ----- 1636
223 QY HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyVal 536
224 DB ----- 1636
225 QY ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
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1636 DB ----- 1636
557 QY ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
1637 DB -----GGACCGCATGAGCCCTCGCGCTCGCGCTGAGTGGCTGCTACCGAT 1684
577 QY PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
1685 DB TTCTTGCAGGCGCGGCGACCGCGCTACGTGGGGTCTACTTCGACGGGCTGCTGCAC 1744
597 QY ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
1745 DB CCAGACTGTGTGCCCTCCCGTTCGCGTCCCGCTCTCTCTCCCTGCCCTCGCAGCTG 1804
617 QY ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
1805 DB CCGGCTTCTCGATGACACTGCAGGAGGCTGCTCCACTCCCGGGGCGACCGCGGAC 1864
637 QY ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
1865 DB CCGGTGGAAACGAGTGCAGGCGCTGCGGTCCCGCTCGACAGCTGTACTTCTAGCTCG 1924
657 QY GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
1925 DB GAAGCCCGAGGCTGCTCGGAGGAATGGACCTGGACCTGCACCTACACTAGAA 1978
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RESULT 10

AX360309 LOCUS AX360309 2022 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0204519.

AX360309 ACCESSION

AX360309.1 GI:18675811

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Gao,Z.

TITLE Murine cytokine receptor

JOURNAL Patent: WO 0204519-A 3 17-JAN-2002;

Zymogenetics, Inc. (US)

FEATURES

Location/Qualifiers

source

1..2022

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/notes="This degenerate nucleotide sequence encodes the

amino acid sequence of SEQ ID NO:2."

ORIGIN

Alignment Scores:

Pred. No.: 1.75e-233 Length: 2022

Score: 2666.00 Matches: 484

Percent Similarity: 71.8% Conservative: 0

Best Local Similarity: 71.8% Mismatches: 190

Query Match: 74.0% Indels: 0

DB: 2 Gaps: 0

US-10-719-202-2 (1-674) x AX360309 (1-2022)

QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20

DB 1 ATCCNGTWSNTGGTYYTYNTWSNTGNCYNTGNGNNGNAAACNGTNGTNGTWSN 60

QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40

DB 61 YTNGBMGNTNATGCAACCCARGAYACNGCNGMTGYWSNTGNGNTWSNTGYCAY 120

QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60

DB 121 YTNTEGGAGGNGAYGTNTGTNTGTYTNCNGGNGWSNYTNCARWSNGCNCNGCNGT 180

61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 181 YTNCTGCCNACNMGNNTNCAACACNGARYTNGTNTNMGNTGYCCNCAARAACNGAYTGY 240
 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisThrAlaGluProGlu 100
 241 GCNTNMGNTNMGNTGNTGNTNCAVYTNCGTNCATGCAAGCNCAYTGGCGNARCCNGAR 300
 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgGlnSerAlaSerLeuGlnAlaGln 120
 301 GARGCGNGAARWSNGAYWNSGARYTNCARGARWSNMGNAAAGCNSNTNCAACGNCAR 360
 121 ValValLeuSerPheGlnAlaValProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
 361 GTNGTNTNWSNTTYCARGCNTAYCCNATHGNCNMGNTGYCNCYNTNMGNTNCAAGTNT 420
 141 ProAlaSerLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 421 CCNGCNGAYTNGTNCARCCNGCNGARWSNGTNGNWSNGCNGTNTTYGATGYTGYGAR 480
 161 AlaSerLeuGlyAlaGluValGlnIleThrSerTyrThrLysProArgTyrGlnLysGlu 180
 481 GCNWSNTYNGGCGNARGTNCARATHGGSNTAYACNAARCCNMGNTAYCARAARGAR 540
 181 LeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer 200
 541 YTNAAAYTNACNARCARVTCNCGAYGNGAYAAAYGTYNTNCAACNTNMGNTNCAAGT 600
 201 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer 220
 601 GARGARCARGAYTYTWSNTTYTNTNAYTNMGNCNCCNCGAYGNTNCAAGTNTNCAAGT 660
 221 LeuTyrTyrLeuAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 240
 661 YTNGTGTAAARAYTNACNGCNCARAAVATHACNTNAAAYCAVACNAGAYTNGTNT 720
 241 ProCysLeuCysIleGlnValThrSerLeuGluProAspSerGluArgValGluPheCys 260
 721 CCNTGYTNTGYATHCARGTNTGGSNTNNGARCCNCGAYWNSGARGMGTNGARTTYTGY 780
 261 PropheArgGluAspProGlyAlaHisArgAsnLeuTyrHisIleAlaArgLeuArgVal 280
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 281 LeuSerProGlyValThrGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 300
 841 YTNWSNCCNGGNTGTGGCARYTNGAYGNCNCTGYTYTNCNCGNAAAGTNTNCAAGT 900
 301 CysThrGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnLys 320
 901 TGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCYNTNGTNCNCCNCGTNCNCAAR 960
 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
 961 AAYGCNACNTNAAAGARCCNCGAYTTCARYTNGTNGCNGCNCAYCCNAAAYTNTGY 1020
 341 ValGlnValSerThrThrGluLysValGlnLeuGlnAlaCysSerThrAlaAspSerLeu 360
 1021 GTNCACTNWSNACNTGGGARAARGTNCARYTNCNCGTNGYSNTGGGNGAYWNSYTN 1080
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 1081 GGNCNCTTYAARGAYGAYTYTNGTNGTNGATGAARACNCGNTNAAAYAAACNWSN 1140
 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
 1141 GTNTGYCNYTNGARCCNWSNGGNTGYACNCTNTNCCNWSNATGGCNGNWSNACNMGNCN 1200
 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTyr 420
 1201 GCNMGNTYNGGARGARYTYTNCARGAYTYTNGWNSNCAICARTGYATGCARYTNTGG 1260
 421 AsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg 440

1261 AAYGAYGAAATATGGNWSNTNTGGCGNTGYCCNATGGAYAAARTAYATHCAVMGNMGN 1320
 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePhePheLeuLeu 460
 1321 TGGGTNTGTNTGGTNGTNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNT 1380
 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
 1381 YTNAAARAGAYMGNMGNNAARGCNGMGNMGWSNMGACNCGNTNTNTNTNCAWNSN 1440
 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
 1441 GCNAYGCGCNGGNTAYGARMGNTGNTGNGCNGNTNCGNWSNCGNTNTNCAWNSN 1500
 501 ProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
 1501 CCNTNMGNTGNGTNGAYTNTGGWSNMGNGARGTYTNWSNCGNCAAYGNGCNYTN 1560
 521 AlaTrpPheHisGlnArgArgGlyLeuGlnGluGlyGlyValValIleLeuLeu 540
 1561 GCNTGGTTCAYCAYCARMGNMGNGNATHYTNCARGGNGGNGTNGTNTNTHYTNTN 1620
 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
 1621 TTYWSNCCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCARACNGTNGARCCN 1680
 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
 1681 GGCNCNCAAYGAYGNTNCGCNGTGGTYWNSNTGYTNTNCCNGAYTNTTYTNCARGN 1740
 581 ArgAlaThrGlyArgTyrValGlyValThrPheAspGlyLeuLeuHisProAspSerVal 600
 1741 MNGCNCNCGNMGTAYGTNGGNTTAYTYGAYGNTTYTNTNCAYCNCNAYWNSGNTN 1800
 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
 1801 CCNWSNCCNTTYTNGTNGCNCNTNTTYTWSNTNCCNACNARYTNCNCGNTTYTNTN 1860
 621 AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
 1861 GAYGNTNCAARGGNGNTGYWSNACNWSNCGNMGNCNCGNCGAYMGNGTNGARMGN 1920
 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
 1921 GTNACNCAACGNTNMGNWSNCGNTNGAYWNTGYACNWSNWSNWSNWSNWSNWSN 1980
 661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
 1981 TGYTGYGARGARTGGAYTNGGNCNTGYACNCACTNGAR 2022

RESULT 11
 AX360312
 LOCUS AX360312 2094 bp DNA linear PAT 13-FEB-2002
 DEFINITION Sequence 6 from Patent WO0204519.
 ACCESSION AX360312
 VERSION AX360312.1 GI:18675814
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 1
 REFERENCE
 AUTHORS Gao,Z.
 TITLE Murine cytokine receptor
 JOURNAL Patent: WO 0204519-A 6 17-JAN-2002;
 ZymoGenetics, Inc. (US)
 FEATURES
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 1..2094
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5."

Db 1981 MGNCTGARMGNTNACNARGCNYTNMGNSNGCNYTNGAYWSNTGYACNWSNWSN 2040

Qy 657 GluAlaProGlyCysGluGluTrrAspLeuGlyProCysThrThrLeuGlu 674
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Db 2041 GARGCNCNGGNTGYTGARGARTGGGAYTTNGCNCNTGYACNACNYTNGAR 2094
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RESULT 12

LOCUS AX350978 2094 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 12 from Patent WO0190358.

ACCESSION AX350978

VERSION AX350978.1 GI:18616354

KEYWORDS

SOURCE unidentified

ORGANISM unclassified sequences.

REFERENCE 1

AUTHORS Gorman, D.M.

TITLE Mammalian receptor proteins; related reagents and methods

JOURNAL Patent: WO 0190358-A 12 29-NOV-2001;
SCHERING CORPORATION (US)

FEATURES
source Location/Qualifiers

1..2094

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

/note="rodent; surmised Mus musculus"

ORIGIN

Alignment Scores:

Pred. No.: 8,386-231 Length: 2094

Score: 2637.00 Matches: 483

Percent Similarity: 69.2% Conservative: 0

Best Local Similarity: 69.2% Mismatches: 191

Query Match: 73.1% Indels: 24

DB: 2 Gaps: 1

US-10-719-202-2 (1-674) x AX350978 (1-2094)

Qy 1 MetProValSerTrrPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
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Db 1 ATGCCNGTNWSNTGGTYYTNTYTNWSNTNGCNYTNGNMGNAAYCCNGTNGTNGTNGSN 60
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Qy 21 LeuGluArgLeuMetGluProGlnAepThrAlaArgCysSerLeuGlyLeuSerCysHis 40
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Db 61 YTNARGMGNTYATGGARCNCARGAYACNCGNMGNTGYWSNTYNGGNTYNSNTGYCAY 120
|||||

Qy 41 LeuTrrAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
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Db 121 YNTGGGAYGGNGAYGTNTYTYTNCNCGNWSNTYTCARWSNCGNCGNCGTNGTNG 180
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Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
|||||

Db 181 YTNCTNCNACNMGNTYTCARACNGARYTNGTNTYTMGNTGYCCNCARAACNGAYTGY 240
|||||

Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrrAlaGluProGlu 100
|||||

Db 241 GCNYTNGTGTNMGNTNGTNGTNCAYTNGCNGTNGTNCAYGGNCAYTGGCGNARGCNCAR 300
|||||

Qy 101 GluAlaGlySerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
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Db 301 GARGCNGGNAARWSNGAYWSNGARYTNCARGARWSNMGNAAYCCNWSNTYTCARCGNCAR 360
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Qy 121 ValValLeuSerPheGlnAlaTrrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
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Db 361 GTNGTNTYTNWSNTTYCARGCNTAYCCNATHGCMGNTGYGCNTYNTYNGARGTNCARGTIN 420
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Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValCysSerAlaValPheAspCysPheGlu 160
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Db 421 CCNCGNAYTNGTNCARCGNCGNARGWSNGTNGNWSNCGTNTTYGATGTGTYTGAR 480
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Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrrSerTrrThrLysProArgTrrGlnLysGlu 180
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Db 481 GCNWSNTYNGCNGARGTNCARATHGTGWSNTAYACNAARCCNMGNTAYCARAARGAR 540

Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
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Db 541 YTNAAAYTNACNARCARYTNCNCGAYTYGWMGNGNTNGARGTNGMGNGAYWSNATHCAR 600
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Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
|||||

Db 601 WSNTGYTGGTNTYCNCTGGYTAAAYGTWWSNACNGAYGGNGAYAAAYTNTYTNACN 660
|||||

Qy 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTrrLeuArgProValProAsp 216
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Db 661 YTNCGYTWSNGARGARGCARGAYTYYTWSNTTYTNTAYTNTMGNCNCGTNGCNGAY 720
|||||

Qy 217 AlaLeuLysSerLeuTrrTrrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
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Db 721 GCNYTNAARWSNTYNTGGTAYAAARAAAYTTCNCGNCGNCARAAYATHACNTYTNAAAY 780
|||||

Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrrSerLeuGluProAspSerGluArg 256
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Db 781 ACNGAYTNGTNCNCTGGTYYTNGTGYATHCARGTNGGWSNTYNGARGCNGAYWSNGARMGN 840
|||||

Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrrHisIleAla 276
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Db 841 GTNGARTTYTGYCCNTTYVMNGARGAYCCNCGNCGNCAYMGNAAYTNTTGGCAYATHGNC 900
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Qy 277 ArgLeuArgValLeuSerProGlyValTrrGlnLeuAspAlaProCysCysLeuProGly 296
|||||

Db 901 MGNYTMGNTYTNWSNCCNGGNTGTGGCARYTNGAYGNCNCGTGTGTGTTCNCGN 960
|||||

Qy 297 LysValThrLeuCysTrrGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
|||||

Db 961 AARGTNACNYTNTGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNYTNGTNCNCGN 1020
|||||

Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
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Db 1021 GTNCCNCARAARAAAYGCNACNGTNAAYGARCNCARGAYTYYCARYTNGTNGCNGNCAY 1080
|||||

Qy 337 ProAsnLeuCysValGlnValSerThrTrrGluLysValGlnLeuGlnAlaCysSerTrr 356
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Db 1081 CCNAAAYTNTGYTNCARGTWNACNTGGGARAARGTNCARYTNCARGCNTGYTNTGG 1140
|||||

Qy 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
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Db 1141 GCNGAYWSNTYNGCNCNTTYAARGAYGAYATGYTNTYNTNGTNGARATGAARACNGGNTN 1200
|||||

Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
|||||

Db 1201 AAYAAAYACNWSNGTNTGYCNYTNGARCCNWSNGNTGYACNCCNYTNCNWSNATGGCN 1260
|||||

Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuGlnAspPheArgSerHisGlnCys 416
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Db 1261 WSNACNMGNGCNCNMGNTYNGNARGARYTNTYTCARGAYTYYMGNSNCAAYCARTGY 1320
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Qy 417 MetGlnLeuTrrAsnAspAspAsnMetGlySerLeuTrrAlaCysProMetAspLysTrr 436
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Qy 437 IleHisArgArgTrrValLeuValTrrLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
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Db 1381 ATHCAYTMGNTMGNTGGGTNTGTNGTNGTNGTNTGYTNTYNTYTCNCGNCGCNYTNTTY 1440
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Qy 457 PhePheLeuLeuLeuLysLysAspArgGlyAlaAlaArgGlySerArgThrAlaLeu 476
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Db 1441 TTTTTTYTNTYTNARAARGAYMGNGNARGCNGNCGNMGNGNWSNMGNACNGCNYTN 1500
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Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTrrGluArgLeuValGlyAlaLeuAlaSerAla 496
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Db 1501 YTNNTYTCAYWSNCGNCGAYGGCNGGNTAYGARMGNTYNTGTNGCNGCNYTNGCNSNGCN 1560
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Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrrSerArgArgGluLeuSerAla 516
|||||

Db 1561 YTNWSNCARATGCCNTYTNMGNTNGCNGTNGAYTYYTGTGWSNMGNGNARGARYTNWSNCGN 1620
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Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgIleLeuGlnGluGlyGlyVal 536
 Db 1621 CAYGGGCGNYTNGCNGTGGTTCAYCAYCARGMNGMGNATHYTNCAARGAGGNGGNGTN 1680
 Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
 Db 1681 GTNATHYTNNTYTNWSNCCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCA 1740
 Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
 Db 1741 ACNGTNGARCCNGGNCNCAYGAGCNYTNGCNGTNGGTYNWSNTGYTNCCNGAY 1800
 Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTrpPheAspGlyLeuLeuHis 596
 Db 1801 TTYTNTCARGGNGMNGCNCAGNGMNTAYGTNGGNGTNTAYTTYGAYGGNYTNTNCAY 1860
 Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
 Db 1861 CCNGAYWSNCTNCCNWSNCCNTTYMNGTNGCNCNTTNTTYSNTNCCNWSNCARYTN 1920
 Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
 Db 1921 CCNGCNTTYTNGAYGNYTNCARGGNGTNGYWSNACNWSNCGNMGNCNGCNGAY 1980
 Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
 Db 1981 MNGTNGARGMNGTNCACARGCNYTNMNGWSNCGNYTNGAYWSNTGYACNWSNWSN 2040
 Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
 Db 2041 GARGCNCNGGNTGYTGYGARGARTGGGAYTNGGNCNTGYACNACNYTNGAR 2094

RESULT 13
 CS251239
 LOCUS CS251239 2255 bp DNA linear PAT 18-JAN-2006
 DEFINITION Sequence 1 from Patent WO2005123778.
 ACCESSION CS251239
 VERSION CS251239.1 GI:85361012
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE
 1 Presnell, S.R.
 Soluble zcytor14, anti-zcytor14 antibodies and binding partners and
 methods of using in inflammation
 Patent: WO 2005123778-A 1 29-DEC-2005;
 ZymoGenetics, Inc. (US)

FEATURES
 source Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 154..2232
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAJ58197.1"
 /db_xref="GI:85361013"

CDS

GAGPGAGDGT"

ORIGIN
 Alignment Scores: 1.09e-204 Length: 2255
 Pred. No.: 2352.50 Matches: 457
 Percent Similarity: 77.1% Conservative: 66
 Best Local Similarity: 67.4% Mismatches: 136
 Query Match: 65.3% Indels: 19
 DB: 2 Gaps: 5
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 Qy 189 ---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe 207
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ACCESSION CS255725
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Hominidae; Homo.
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AUTHORS Eaton,D.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
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Genetech, Inc. (US)
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Tue Aug 22 11:34:34 2006

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US-10-719-202-2 (1-674) x CS255725 (1-2380)

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Job time : 8953 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 09:00:24 ; Search time 339 Seconds
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5580.209 Million cell updates/sec

Title: US-10-719-202-2

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SUMMARIES

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ALIGNMENTS

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; Sequence 13, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30

QY	302	TripGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnLysAsn	321	645	LeuArgSerAlaLeuAspSerCys-----ThrSerSerSerGluAlaProGly	660
Db	1420	TGGCGGGCTCGGGTGGGGACCCCTGCCAGCCACTGGTCCACCGCTTCTCTGGGAGAT	1479	2494	CTTCAGCCAGCCCTGGATAGCTACTTCCATCCCGGGGACTCCCGCGCGGGA	2547
QY	322	AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysVal	341			
Db	1480	GTCACTGTGGACAAGTCTCTCAGTTCCATTGTGTGAAGGCCACCCCTAACTCTGTGTT	1539			
QY	342	GlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGly	361			
Db	1540	CAGGTGAACAGCTCGGAAGAGCTGAGCTGCAGAGTCTGTGGCTGACTCTCTGGG	1599			
QY	362	ProPheLysAspAspMetLeuValGluMetLysThrGlyLeuAsnAsnThrSerVal	381			
Db	1600	CCTCTCAAGACGATGTCTACTGTGGAGACAGAGGCCCCAGGACACACAGATCCCTC	1659			
QY	382	CysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla	401			
Db	1660	TGTGCTTTGGAACCCAGTGGCTGTACTTCACTACCCAGCAAGCCTCCACGAGGCGAGCT	1719			
QY	402	ArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsn	421			
Db	1720	CGCCTTGGAGAGTACTTACTACAGACCTGCAGTCAGCCAGTGTCTCAGCTATGG---	1776			
QY	422	AspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrlleHisArgArgTrp	441			
Db	1777	GACGATGACTTGGGAGCGCTATGGCGCTGCCCATGGACAAATACATCACAAAGCGCTGG	1836			
QY	442	ValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeu	461			
Db	1837	GCCTCTCGTGTGGCTGGCTGCTCTCTTGGCGCTGCGCTTTCCTCATCTCTCTCTC	1896			
QY	462	LysLysAspArgArgLys-----	467			
Db	1897	AAAAAGGATCATCGCGAAGGGTGGCTGAGGCTCTTGAACAGAGCGTCCGCTCGGGGCG	1956			
QY	468	AlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrlu	487			
Db	1957	GCCTGTGGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG	2013			
QY	488	ArgLeuValGlyValAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaVala	507			
Db	2014	CGCTGTGGTGGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG	2073			
QY	508	LeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArg	527			
Db	2074	CTGTGAGCGCTGTAACCTGAGCGCGCAGGGCGCGTGGCTTGTGTTTCACTGCGCAGCG	2133			
QY	528	ArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSerProAlaAlaValAla	547			
Db	2134	CGCCAGACCTGCGAGAGGCGCGTGGTGTGCTTCTCTCCCGTGGGTGGCG	2193			
QY	548	GlnCysGlnGlnTrpLeuGlnLeuThrValGluPro-----GlyProHisAsp	564			
Db	2194	CTGTGAGCGAGTGGCTACAGATGGGTGTTCGGGCGCGCGCGCGCGCGCGCGCG	2253			
QY	565	AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly	584			
Db	2254	GCCTTCGGCGCTCGCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2313			
QY	585	ArgTyrlValGlyValTyrlPheAspGlyLeuLeuHisProAspSerValProSerProPhe	604			
Db	2314	AGCTACGTGGGGCGCTGTCTGACAGCGCTCTCCACCGACCGCTGACCCCGCTTTTC	2373			
QY	605	ArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGln	624			
Db	2374	CGCACCGTGGCGCTTTCACACTGCCCTCCCAACTGCTGCTGCTGCTGCTGCTGCTG	2433			
QY	625	GlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla	644			
Db	2434	CAGCCTCGCGCGCGCTTCCGGCGCGCTCCAAAGAGAGCGGAGCAAGTGTCCCGGCG	2493			
<p>RESULT 3</p> <p>US-09-747-259-15</p> <p>; Sequence 15, Application US/09747259</p> <p>; Patent No. 6569645</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Genentech, Inc.</p> <p>; APPLICANT: Chen, Jian</p> <p>; APPLICANT: Filvaroff, Ellen</p> <p>; APPLICANT: Fong, Sherman</p> <p>; APPLICANT: Goddard, Audrey</p> <p>; APPLICANT: Godowski, Paul</p> <p>; APPLICANT: Grimaldi, Christopher</p> <p>; APPLICANT: Gurney, Austin</p> <p>; APPLICANT: Li, Hanzhong</p> <p>; APPLICANT: Hillan, Kenneth</p> <p>; APPLICANT: Tumas, Daniel</p> <p>; APPLICANT: Vanlokeren, Menno</p> <p>; APPLICANT: Vandlen, Richard</p> <p>; APPLICANT: Watanabe, Colin</p> <p>; APPLICANT: Williams, P. Mickey</p> <p>; APPLICANT: Wood, William</p> <p>; APPLICANT: Yansura, Daniel</p> <p>; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF</p> <p>; FILE REFERENCE: P1381K1C1P1 (US)</p> <p>; CURRENT APPLICATION NUMBER: US/09747,259</p> <p>; CURRENT FILING DATE: 2000-12-20</p> <p>; PRIOR APPLICATION NUMBER: US 09/311,832</p> <p>; PRIOR FILING DATE: 1999-05-14</p> <p>; PRIOR APPLICATION NUMBER: US 60/172,096</p> <p>; PRIOR FILING DATE: 1999-12-23</p> <p>; PRIOR APPLICATION NUMBER: PCT/US99/31274</p> <p>; PRIOR FILING DATE: 1999-12-30</p> <p>; PRIOR APPLICATION NUMBER: US 60/175,481</p> <p>; PRIOR FILING DATE: 2000-01-11</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/04341</p> <p>; PRIOR FILING DATE: 2000-02-18</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/05841</p> <p>; PRIOR FILING DATE: 2000-03-02</p> <p>; PRIOR APPLICATION NUMBER: US 60/191,007</p> <p>; PRIOR FILING DATE: 2000-03-21</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/07532</p> <p>; PRIOR FILING DATE: 2000-03-21</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/15264</p> <p>; PRIOR FILING DATE: 2000-06-02</p> <p>; PRIOR APPLICATION NUMBER: US 60/213,087</p> <p>; PRIOR FILING DATE: 2000-06-22</p> <p>; PRIOR APPLICATION NUMBER: US 09/644,848</p> <p>; PRIOR FILING DATE: 2000-08-22</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/23328</p> <p>; PRIOR FILING DATE: 2000-08-24</p> <p>; PRIOR APPLICATION NUMBER: US 60/242,837</p> <p>; PRIOR FILING DATE: 2000-10-24</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/30873</p> <p>; PRIOR FILING DATE: 2000-11-10</p> <p>; PRIOR APPLICATION NUMBER: US 60/253,646</p> <p>; PRIOR FILING DATE: 2000-11-28</p> <p>; PRIOR APPLICATION NUMBER: PCT/US00/32678</p> <p>; PRIOR FILING DATE: 2000-12-01</p> <p>; NUMBER OF SEQ ID NOS: 39</p> <p>; SEQ ID NO 15</p> <p>; LENGTH: 2138</p> <p>; TYPE: DNA</p> <p>; ORGANISM: Homo Sapien</p> <p>US-09-747-259-15</p>						<p>Alignment Scores:</p> <p>Pred. No.: 5,51e-21 Length: 2138</p> <p>Score: 316.50 Matches: 182</p> <p>Percent Similarity: 35.3% Conservativity: 68</p>

Best Local Similarity: 25.7%				Matches: 269			
Query Match: 8.8%				Indels: 192			
DB: 3				Gaps: 30			
US-10-719-202-2 (1-674) x US-09-747-259-15 (1-2138)							
Qy	14	AtqAspPro-ValValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCy	33	Qy	341	lGlnValSerThrTrpGluLysValGlnLeuGlnAlaCys-	356
Db	407	AGAAATCCAAAGAGCTTCCACATTCAAGTTCTATAGGAGACACAGATGCCAGCACTG	466	Db	1128	-CAAGTTCTCTTTTGGAAACAG-----CAGCCATGTTGAATGCCCCACAGACTG	1177
Qy	33	sSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLe	53	Qy	356	pAlaAspSerLeu-----GlyProPheLysAspAspMetLe	368
Db	467	CTCAGA-GGAAGCTGCTCGTC-----GTCCCTGTCTGAGAGAGCCAT	513	Db	1178	GGTCTCTCATCTCTGGAATGTAAAGCATGGATATCAAGCCAGCCAGCTGATTTCTTCACT	1237
Qy	53	uGlnSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeuValLeuAr	73	Qy	368	uLeuValGluMetLeuThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-SerG	388
Db	514	CACATTTCCATCCCTCCCGACATCTCCACAGG-----GACTTCGCTCTAAA	564	Db	1238	TTCTCTCAAGATGCATGCCACCTTCAG-----TGCTGCTGGAGGCTCCCGAC	1285
Qy	73	gCysProGlnLysThrAspCysAlaLeuArgValArgValValHisLeuAlaValHi	93	Qy	388	lyCys-----ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyG	405
Db	565	AGGACCC-----AACCTTCGGATCCAGACATGGGAAGTCTT	603	Db	1286	GCTTGGGGCAGGACACTTTTGGTGCCTCCCGTGATACCTGTGCAGCCAGCCCGGGGCTCAA	1345
Qy	93	sGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSerGluLeuGlnGluSerAr	113	Qy	405	luGluLeuLeuGlnAsp-----PheArgSerHisGlnCysMetGlnLeuT	420
Db	604	CCAGATTGGACT-----CACAAAGGCATGAGAGCC-GAG-----	639	Db	1346	GCCCATGTGCTATAGACCTCATTCCTCTCTGAGGCCAGGGTGTGTCTCTGGTGT	1405
Qy	113	gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCy	133	Qy	420	zPaAsnAspAspAsnMetGlySerLeuTrp-----AlaCysProMetAspLysTyrI	437
Db	640	-----TTCTCTCTTGTATTGTCTGCTGAGGCCCGCGGC	671	Db	1406	GGCGGTCAAGT---GTCCAGTTTGCCTTGAAGCACCTCTTGTGTCCAGATGTCTTTACA	1462
Qy	133	sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySe	153	Qy	437	leHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPheP	457
Db	672	TATTCGGGTGACCATA-----	687	Db	1463	GACACCTGGG-----CTCTTGATCTTGGCACTGTGTGGCCCTCTCACCTACTGGGTG	1516
Qy	153	zAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluValGlnIle-----	169	Qy	457	hePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGly-----SerArgThrAlaL	476
Db	688	-----TCTTCAGGCCCTGAGGTGAGCTGAGCGTCTTTGTCA	722	Db	1517	TTGTTCTGGCCCTCACCTGCGCGGCCACACTGTAGCGCCCGGCCAGCGCGCCAGTGC	1576
Qy	170	-----TrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLeuThrGlnLeuPr	188	Qy	476	euleLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerA	496
Db	723	CCAGTGGGCA-----	732	Db	1577	TCCTCTTCAGCGCGGAGCTCGAGGGCGAGCGCGCTGTGTGGAGCGCTGGCTGAAC	1636
Qy	188	oAspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluAspPheSerPheLe	208	Qy	496	laleuSerGlnMet-----ProLeuArgValAlaValAspLeuTrpSerArgArg	513
Db	733	-----CTGAGTGTGAAGAGCTGAGCAGCTCCCTATGATGTCCAG-----	771	Db	1637	TGCTACGCGCAGCGCTGGCGCGCGCGAGCTGTCTGTGACCTGTGTGGAGGGAGGC	1696
Qy	208	uLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThrGl	228	Qy	513	luleuSerAlaHisGlyAlaLeuAlaLeuAlaTrpPheHisGlnArgArgArgIleLeuGlnG	533
Db	772	-----AAAAATTGTGTGG	785	Db	1697	ACGTGCGCGCGTGGGCGCGCTGCGTGGCTCTGGCGCGCGCGAGCGCGCTAGCGGG	1756
Qy	228	yProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTr	248	Qy	533	luGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpL	553
Db	786	GGGCCACACTGTAGAGCTGCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATC	845	Db	1757	AGCAGGGCACTGT	1791
Qy	248	pSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAl	268	Qy	553	euglnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV	573
Db	846	CTACCTGCAAGAGGACACTGTGAGGGCGCAAAATGTCCCTTCCAGAGCTGGCCAGAGC	905	Db	1792	--GACCTTGGCCCGGTTCAGC---GGCCCGAGCCCCCGCGCGCTGTCTGCC---	1842
Qy	268	aHis---ArgAsnLeuTrp-----HisLeuAlaArgLeuArgValLeuSerProGl	284	Qy	573	allLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspG	593
Db	906	CTATGGCTCGGACTTCTGGAAGTCACTGACCTTCACTGACTACAGCCAGCAGCATCAGAT	965	Db	1843	-----CTGCTCCAGCTGCGCGCGCGCGCTGTCTGTCTGTCTTACTTTCAGTC	1891
Qy	284	yValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl	304	Qy	593	lyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuP	613
Db	966	GGTCATGGCCCTGACACTCGCTGCCACCTGAAGCTGGAAGCTGCTGTGCCAGAGGCA	1025	Db	1892	GCCTCTGCGCCCAAGGCGACATCCCCCGCGCGCTGTGTGTGTGTGTGTGTGTGTGT	1951
Qy	304	aProAspGlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaThrVa	324	Qy	613	roThrGlnLeuProAlaPheLeuAspAlaLeuGlnGly-----GlyCysSerThrS	630
Db	1026	CGACTGGCATACCTTTGCAAGACCTC-----CCGATGCCAGGC	1067	Db	1952	TGGCGACCTGCGCGCTGT	2011
Qy	324	laenGluProGlnAspPhe-----GlnLeuValAlaGlyHisProAsnLeuCysVa	341	Qy	630	erAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuA	650
Db	1068	TCGAGAGTCAGATGGGTGTATGTTTTGGAGAGGTGGACCTGCACCCCCCAGCTCTGCTT	1127	Db	2012	GCTGGGCGCGCTTGGGCG	2056
				Qy	650	spSerCysThr-----Sers	655
				Db	2057	AGCTGTGCAGCGCGCTTGAACGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2116

[illegible]

Tue Aug 22 11:34:35 2006

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; LOCATION: (1)... (681)
US-09-893-737-327

Alignment Scores:      1.43e-09      Length:      681
Pred. No.:            193.50      Matches:      73
Score:                42.2%      Conservative: 21
Percent Similarity:   32.7%      Mismatches:  102
Best Local Similarity: 5.4%      Indels:       27
Query Match:         3          Gaps:         7
DB:

US-10-719-202-2 (1-674) x US-09-893-737-327 (1-681)

QY 438 HisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhePhe 457
Db 31 TACAGACACCTGGGGCTCTTATCTGTCATCTGTCCTCTCCCTCCTACTGCGGT 90
QY 458 PheLeuLeuLeuLysAspArgArgLysAlaAlaArgGly---SerArgThrAlaLeu 476
Db 91 GTTCTGGCCCTCACCTGGCGGCGCCACAGTCAGCGCGCGCCAGCGCGCGAGTCTC 150
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 151 CTCCTGCACCGCGCGACTCGGAGCGCGAGCGCGCGCTGGTGGAGCGCTGCTGAAGT 210
QY 497 LeuSerGlnMet-----ProLeuArgValAlaValAspLeuTrpSerArgArgGlu 513
Db 211 CTACGGGCGAGCGCTGGCGGCGCGCGCGAGCTGATCGTGGACCTGTGGAGGGAGGCAC 270
QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleuGlnGlu 533
Db 271 GTGGCGCGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 534 GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
Db 331 CAGGGGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 554 GlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysVal 573
Db 364 GACCTTTCGCGCGTACG---GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414
QY 574 LeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGly 593
Db 415 -----CTGTCCACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 465
QY 594 LeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuPro 613
Db 466 CTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 525
QY 614 ThrGlnLeuProAlaPheLeuAspAlaLeuGlnGly-----GlyCysSerThrSer 630
Db 526 CGCGACCTGCGCGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 585
QY 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 586 TGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 630
QY 651 SerCysThr 653
Db 631 CTGTGCGCG 639

RESULT 7
US-08-620-694A-1
; Sequence 1, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
```

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; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-08-620-694A-1

Alignment Scores:      1.5e-06      Length:      3288
Pred. No.:            174.50      Matches:      119
Score:                31.6%      Conservative: 65
Percent Similarity:   20.4%      Mismatches:  192
Best Local Similarity: 4.8%      Indels:       207
Query Match:         2          Gaps:         26
DB:

US-10-719-202-2 (1-674) x US-08-620-694A-1 (1-3288)

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Db 316 AAAAAACCTGACCCCGCTCTTCCCAAAACATCTATATCAATCTTAGTGTTCCTCTTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGCGAGAAATTAGTCCCTGTGTTCATGTTGAG---TGGACCTCGACGACAGATGCC 432
QY 254 -----SerGluArg 256
Db 433 AGCATCTCTGACCTCGAGGTGTCGCTCGTCCGTCGAGCTGAGTGAACCAATGAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAAGTTTC---CAGTTTCTGTCTCCATGCTCGACGATCACCCTAAGCGGTGCGG 549
QY 275 IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
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Db 550 TTTCTTCAGCCACTTTGGTAGACTCTGGC----- 582
Qy 294 LeuProGlyValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGAGATGATGAAGTACTGTT-----CACCACCTG 612
Qy 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCATCCCTGATGGGACCCCAACCAAAATCCA----- 652
Qy 333 lAlaGlyHisProAsnLysValGlnValSerThr----- 345
Db 653 -----AGATCATCTTTGCTGCTGCTGAGCAGCAGCAAGATGAAGTACTACCTCA 705
Qy 346 -----TTPGLYValGlnLeuG1 352
Db 706 TGCCTGAGCTCAGCAGCCCTTTGGGATCCCAATCATCTGAGGACCTTGGACACACAG 765
Qy 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuValGluMe 372
Db 766 CATCTGCGAGTGG----- 778
Qy 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
Db 779 -----ACTTCACCTCTGGGAATGAATCCACCCCTACCAGGCTCTG 819
Qy 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
Db 820 CTGGAAGTTCTCCGACTCAGACACCACTGCTTGTATGTCGTAAACAAATATTT 879
Qy 408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspMetGlySerLe 428
Db 880 GCGCCAGGCGAAGAATCCATCAGCGAGTAAATGTGCATTC-ACTCTAAGCAAGTT 938
Qy 428 u---TrpAlaCys----- 431
Db 939 TCACTGTGTGCTGCCATCACCAGTGCAGGTCAGCCCTTCTTCAGCAGCTGCCATAATGA 998
Qy 431 ----- 431
Db 999 CTGTTTGAGACAGCTGTGATGTCGCCCTGCCAGTAATCTCAAAATACCACAGTTCCAA 1058
Qy 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
Db 1059 GCCAGTTGCAGACTACATT---CCCTGTGGGTGATGGCTCATCATCTCATCGCCAT 1115
Qy 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
Db 1116 TCTGCTGTGGATCTGTCATCGTGTGATCATCTGTATGACCTGGAGGCTTTCTGGCGC 1175
Qy 463 sAspArgArgLysAlaAlaArgGlySer----- 472
Db 1176 CGATCAAGAGAAACATGCTGATGATGATCCAAATCAATGCGATCTTGGCCGTAGCAGACCT 1235
Qy 473 -----ArgThrAlaLeuLeuHisSerAlaAspGlyAlaG1 485
Db 1236 GACTCCCCCACCCTGAGGCCAGAGGCTGATGCTGCTACTGCGCCGACACCCCT 1295
Qy 485 YTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerGlnMetProLeuArgVa 504
Db 1296 CTATGTGGAGTGTGCTCTAAAGTTCCGCCAGTCTCTGATCCTGATCCTGCTGGCAGT 1355
Qy 504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
Db 1356 AGCCCTTGACTCTCTGAAAGCAGAGGTTATCTCTGAGGTGGGGTCAATGACCTGGGTGAG 1415
Qy 524 sHisGlnArgArgIleLeuGlnGluGlyValValValIleLeuLeuPheSer----- 542
Db 1416 CCGACAGAGCAGAGATGTTGGAGACCACTCCAAATCATCATCTCTGTGTTCCCGAGG 1475
Qy 543 -----ProAlaAlaValAlaGlnCy 549
Db 549 -----

Db 1476 CACCCAGCAAACTGGAAAGCTATCTTGGTTGGCTGAGCCCTGCTGTCTCAGCTACGGT 1535
Qy 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
Db 1536 TGACCACTGG-----AAGCTGCT---GGGACCTTTTCACTGCAGC 1574
Qy 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
Db 1575 CATGAACATGATCTCTCCAGACTTCAAGAGGCCAGCTGCTTGGCACCCTACGTGTTG 1634
Qy 589 lTyPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
Db 1635 CTACTTCTAGTGTCATCTGTAGTGAGAGGATGTCCTCCAGCCTCTTCAACATCACTCCAG 1694
Qy 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
Db 1695 GTACCCACTCATGACAGATTTGAGGAGGTTTACTTCCGATCCAGGACCTGGAGATGTT 1754
Qy 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCCGCGCGATGTCACCATGTCTCAGAGAGCTCACAGGGGACAAATTACCTGCAGAGCCC 1814
Qy 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerGluAlap 659
Db 1815 TAGTGCCCGCAGCTCAAGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAAACCCAGTGCCC 1874
Qy 659 ro 659
Db 1875 CG 1876
RESULT 8
US-09-022-255-1
; Sequence 1, Application US/0902255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Farnlow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

Tue Aug 22 11:34:35 2006

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;
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-09-022-255-1

Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-022-255-1 (1-3288)
QY 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAACCTGACCCCGCTCTCCCAAAACATCTATATCAATCTTAGTGTTCCTCTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGGAGAAATAGTCCCTGTGTTCATGTTGAG---TGGACCTCGACGACATGCC 432
QY 254 -----SerGluArg 256
Db 433 AGCATCCTGTACTCAGGGGTGAGAGTGTCCGTCTGACGTGAACACCAATGAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAGGTTTC---CAGTTTCTGTCATGCTGCAGCATCACCGTAAAGCGGTGGCG 549
QY 275 IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCys 293
Db 550 TTTTCTCTTCAGCCACTTTGTGGTAGATCTCTGGC----- 582
QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTATGAAGTACTGTT-----CACCACTG 612
QY 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCATCTCCTGATGGGACCCCAACACCAATCCA----- 652
QY 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
Db 653 -----AGATCATCTTTGTGCTGCTGTGAGGACAGCAAGATGAAGATGACTACTCA 705
QY 346 -----TrpGluLysValGlnLeuG1 352
Db 706 TGCCTGAGCTCAGGACGCTTTGGGATCCCAACATCATCTGTGGAGACTTGGACACACAG 765
QY 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
Db 766 CATCTGCAGTGG----- 778
QY 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
Db 779 -----ACTTCACCTGTGGGAATGAATCCACCCCTACCGAGTCTGT 819
QY 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
Db 820 CTGGAAGAGTTCTCCGACTCAGAGNACCACGAGTGTCTTTGATGTCTGTAAACAATATTT 879

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QY 431 ----- 431
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QY 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
Db 1059 GCCAGTTGCAGACTCATTT---CCCTGTGGGTGTATGGCTCATCACATCATCGCCAT 1115
QY 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLys 463
Db 1116 TCTGCTGGTGGGATCTGTCTCATCGTGTGATCATCTGTATGACCTGGAGGCTTTCTGGCGC 1175
QY 463 sAspArgArgLysAlaAlaArgGlySer----- 472
Db 1176 CBATCAAGAGAAACATGTCATGACTCCAAAATCAATGGCATCTTGCCCGTAGCAGACCT 1235
QY 473 -----ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaG1 485
Db 1236 GACTCCCCCACCCTGAGGCGCCAGGAAGTCTGGATCTGTACTTCGCGCCACACCCCT 1295
QY 485 yTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerGlnMetProLeuArgVa 504
Db 1296 CTATGTGGAGTGTGTCTTAAAGTTGCGCCAGTCTCTGATCATCTGCTGTGGCTGAAGT 1355
QY 504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
Db 1356 AGCCCTTGACCTCTGGAGAGCAGGTTATCTCTGAGTGGGGTCTGATGCTGGTGAG 1415
QY 524 sHisGlnArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSer----- 542
Db 1416 CCGACAGAAGCAGGAGATGTTGGAGAGCACTCCAAAATCATCATCTGTGTTCGCGAGG 1475
QY 543 -----ProAlaAlaValAlaGlnCy 549
Db 1476 CACCAACAAAGTGAAGACTATCTTGGGTGGGCTGAGCCTGTCTCCAGTACGCTG 1535
QY 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
Db 1536 TGACCACTGG-----AAGCCTGCT---GGGGACCTTTTCACTGCGACG 1574
QY 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
Db 1575 CATGAACATGATCTCTGCCAGACTTCAGAGGCCAGCCTGCTTCGGCACCTAGCTGTGTTG 1634
QY 589 lTrpPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
Db 1635 CTACTTCAGTGGCATCTGTAGTGAGGGGATGTCCCGACCTCTTCAACATCATCCTCCAG 1694
QY 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
Db 1695 GTACCCACTCATGGACAGATTTGAGAGGTTTACTTCGGATCCAGGACCTGGAGATGTT 1754
QY 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCCGCCCGATGTACCATGTCCAGAGAGTCTCAGGGGCAATTTACTCGAGAGCCC 1814
QY 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaP 659
Db 1815 TAGTGCCCGGAGCTCAAGGAGGTGTGCTTAGTTCCAGAGTGTGCTTCCAGAGTGCAC 1874
QY 659 xo 659
Db 1875 CG 1876

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RESULT 9

TELECOMMUNICATION INFORMATION:

504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
1356 AGCCCTTGACCTCTCGAAGACGAGGTTATCTCTGAGGTGGGGTCTATGACCTGGGTGAG 1415
524 sHisGlnArgArgGlnLeuGlnGlyGlyValValIleLeuLeuPheSer----- 542
1416 CCGACAGAAGCAGGAGATGGTGGAGAGCAACTCCAAATCATCATCTGTGTTCGCGAGG 1475
543 -----ProAlaValAlaGlnCy 549
1476 CACCCAGCAAGTGAAGCTATCTTGGGTGGGCTGAGCCTGCTCCAGCTACGGTG 1535
549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
1536 TGACCACTGG-----AAGCCTGCT---GGGACCTTTTCACTGCAGC 1574
569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVa 589
1575 CATGAACATGATCTCGCCAGACTTCAAGAGCGCAGCTGCTTCGCGACCTACGTTGTTG 1634
589 lTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
1635 CTACTTCAGTGCACTCTGTAGTGAGAGGATGTCGCCGACCTCTTCAACATCACCTCCAG 1694
609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
1695 GTACCCACTCAGGACAGATTGAGGAGGTTTACTTCCGATCCAGGACCTGGAGATGTT 1754
625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
1755 TGAACCCGCGCGATGCACCATGTTCAGAGAGTCAAGGGGACAAATACCTGCAGAGCCC 1814
639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaP 659
1815 TAGTGGCCGCGAGCTCAAGAGAGCTGTGCTTAGGTTCCAGGAGTGCRAACCCAGTGCCC 1874
659 ro 659
1875 CG 1876

RESULT 10
US-08-978-773-1
Sequence 1, Application US/08978773
Patent No. 6083906

GENERAL INFORMATION:
APPLICANT: Trout, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A

US-10-719-202-2 (1-674) x US-08-978-773-1 (1-3288)
Alignment Scores: 1.5e-06 Length: 3288
Pred. No.: 119
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: 26 Gaps: 26
US-10-719-202-2 (1-674) x US-08-978-773-1 (1-3288)
QY 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAAACCTGACCCCGTCTTCCCAAAAACATCTATATCAATCTTAGTGTTCCTCTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCACGGAGAAATAGTCCCTGTGTCATGTTGAG---TGGACCTGCAGACAGATGCC 432
QY 254 -----SerGluArg 256
Db 433 AGCATCCTGTACTCGAGGGTGACAGCTGTCCCTGTCAGCTGAACACCAATGAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAAGTTC---CAGTTTCTGTCCATGTGTCAGCATCACCGTAAGCGGTGGCGG 549
QY 275 lIleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
Db 550 TTTTCTTCAGCCACTTTGTGTAGATCCTGGC----- 582
QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTATGAAGTGACTGTT-----CACCACCTG 612
QY 314 ValProProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCATCCCTGATGGGACCCCAACCAATCCA----- 652
QY 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
Db 653 -----AGATCATCTTTGTGCTGTGAGGACAGCAAGATGAAGATGACTACCTCA 705
QY 346 -----TrpGluLysValGlnLeuG1 352
Db 706 TGGCTGAGCTCAGGACGCTTTGGGATCCCAATCATCTGTCGAGACCTTGGACACACAG 765
QY 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
Db 766 CATCTGGAGTGG----- 778
QY 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389


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US-10-719-202-2 (1-674) x US-09-022-253-1 (1-3288)
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QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGCAGAGAAATAGTCCCTGTGTGATGTTGAG---TGGACCTGCGACAGATGCC 432
QY 254 -----SergluArg 256
Db 433 AGCATCTGTACCTGAGGGTGCAGAGCTGTCCCTCTGCGAGCTGAACCAATAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAAGTTC---CAGTTTCTGTCCATGTGTCAGCATCACCGTAAGCGGTGGCGG 549
QY 275 IleAlaArgLeuArg---ValIleSerProGlyValTrpGlnLeuAspAlaProCysCys 293
Db 550 TTTTCCTTCAGCCACTTTGTGTGATCTCTGCG----- 582
QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTAGTGAAGTGAAGTGT-----CACACACTG 612
QY 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCATCCCTGTATGGGAGCCCAACCAATCA----- 652
QY 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
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QY 346 -----TrpGluLysValGlnLeuG 352
Db 706 TGGCTGAGCTCAGGCGACCTTTGGGATCCCAACATCATCTGTGGAGACCTTGACACAG 765
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Db 766 CATCTGGAGTGG----- 778
QY 372 tLysThrGlyLeuAsnThrSerValCysAlaLeuGluPro-----SerGlyCys 389
Db 779 -----ACTTCACCTGTGGAATGAAATCCACCCCTACAGGTCCTG 819
QY 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
Db 820 CTGGAAGATTCTCCGACTCAGAGACCAACAGCTGCTTTGATGCTGTTAAACAAATATTT 879
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QY 431 ----- 431
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QY 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
Db 1059 GCCAGTTCAGACATACATT---CCCTGTGGGTGTATGGCTCATCATCTATCGGCAT 1115
QY 449 uLeuLeuAlaAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
Db 1116 TCTGTGTGGGATCTGTGATCGTGTGATCATCTGATGATGATGATGATGATGATGATGATG 1175
QY 463 sAspArgArgLysAlaAlaArgGlySer----- 472
Db 1176 CGATCAAGAGAAACATGGTGTGATGACTCCAAAATCAATGCATCTTGGCCGTAGCAGACCT 1235

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RESULT 12
US-09-022-260-1
; Sequence 1, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260

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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-09-022-260-1

Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-022-260-1 (1-3288)

Qy 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAAACCTGACCCCGCTTCCCAAAACATCTATATCAATCTTAGTGTTCCTCTACC 375
Qy 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGCGAGNATAGTCCCTGCTTGCATGTTGAG---TGGACCTGCGACAGATGCC 432
Qy 254 -----SergLuarG 256
Db 433 AGCATCTGTACCTCGAGGGTGCAGAGCTGCTCCGCTCGAGCTGAACACCAATGACGG 492
Qy 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAGTTTC---CAGTTTCTCTCCATGCTGCAGCATCACCCGTAAGCGGTGCGG 549
Qy 275 IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
Db 550 TTTTCCTTCAGCCACTTTGTGTAGATCCTGGC----- 582
Qy 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTATGAGTGACTGTT-----CACCACCTG 612
Qy 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCCATCCCTGTATGGGGACCAACCAAAATCCA----- 652
Qy 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345

653 -----AGATCATCTTTGTCCTGACTGTGAGCAGCAGCAAGATGAAGATGACTACCTCA 705
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706 TGCCTGAGCTCAGGCACGCTTTGGGATCCCAACATCACTGTGGAGACCTTTGGACACACAG 765
352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuValGluMe 372
766 CATCTGGAGTGG----- 778
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779 -----ACTTCACCTGTGGAATGAATCCACCCCTACCAGGTCTCTG 819
389 sThrProLeu---ProSerMetalaserThrArgAlaAlaArgLeuGluGluLeuLe 408
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408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe 428
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939 TCACTGCTGCTGCCATCACCACCTGCAGGTCCAGCCCTCTTCTCAGCAGCTGCCTAAATGA 998
431 ----- 431
999 CTGTTTGAGACACGCTGTGATGTGCCCTGCCAGTAATCTCAATATACACAGATTCCTCAA 1058
432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
1059 GCCAGTTGCAGACTACAT---CCCTGTGGGTGTATGGCCTCATCACATCATCGCCAT 1115
449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
1116 TCTGCTGCTGGGATCTGTCTCATCTGTGATCATCTGTATGATCCTGTGAGGCTTTCTGGCGC 1175
463 sAspArgArgLysAlaAlaArgGlySer----- 472
1176 CGATCAAGAGAAACATGTTGATGACTCCAAATCAATGGCATCTTGGCCGTAGCAGACCT 1235
473 -----ArgThrAlaLeuLeuHisSerAlaAspGlyAlaG1 485
1236 GACTCCCCACCCCTCAGGCCAGGAGGTCTGATCGTCTACTCTGCGCCACACCCCT 1295
485 YTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerGlnMetProLeuArgVa 504
1296 CTATGTGGAGGTGTTCTAAAGTTTCCGCAAGTTCTCTGATCCTGATCCTGTCGCACTGAAGT 1355
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1356 AGCCCTTGACCTCTCGAAGAGCAGGTTATCTCTGAGGTGGGGTCTATGACCTGGGTGAG 1415
524 sHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSer----- 542
1416 CCGACAGAGCAGAGATGTTGGAGAGCAACTCCAAATCATCTCTGTGTTCCCGAGG 1475
543 -----ProAlaAlaValAlaGlnCy 549
1476 CACCAAGCAAGTGGAAAGCTATCTTGGGTGGGCTGAGCCTGCTCTCCAGCTACGGTG 1535
549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
1536 TGACCACTGG-----AAGCCTGCT---GGGGACCTTTTTCATCTGCAGC 1574
569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
1575 CATGAACATGATCTCTCCAGACTTCAAGAGCCAGCGCTGCTTGGCACCCTACCTGTTGTTG 1634
589 lTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
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Db 1635 CTACTTCAGTGGGCACTGTGTAGTGAGAGGGATGTCCCGACCTCTTCAACATCACCTCCAG 1694

Qy 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624

Db 1695 GTACCCACTCATGCAGAGATTGTGAGAGGTTTACTTCCGGATCCAGGACCTGGAGATGTT 1754

Qy 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639

Db 1755 TGAACCGCGCGATGCACCATGTACAGAGCTCACAGGGGACAAATTACTCTGCAGAGCCC 1814

Qy 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlap 659

Db 1815 TAGTGGCGCGCAGCTCAAGGAGGCTGTGCTTAGTTCCAGGAGTGGCAAAACCCAGTCCCC 1874

Qy 659 ro 659

Db 1875 CG 1876

RESULT 13

US-09-022-259-1

; Sequence 1, Application US/09022259

; Patent No. 6191104

; GENERAL INFORMATION:

; APPLICANT: Yao, Zhengbin

; APPLICANT: Spriggs, Melanie

; APPLICANT: Fanslow, William

; TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/022,259

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION NUMBER: 08/620,694

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/410,535

; FILING DATE: 23 MARCH 1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,695

; REFERENCE/DOCKET NUMBER: 2617-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3288 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Mouse

; STRAIN: HVS13 receptor

; FEATURE:

; NAME/KEY: CDS

i LOCATION: 121..2715

US-09-022-259-1

Alignment Scores:

Pred. No.: 1.5e-06 Length: 3288

Score: 174.50 Matches: 119

Percent Similarity: 31.6% Conservative: 65

Best Local Similarity: 20.4% Mismatches: 207

Query Match: 4.8% Indels: 26

DB: Gaps: 3

US-10-719-202-2 (1-674) x US-09-022-259-1 (1-3288)

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Qy 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253

Db 376 CAGCAGGAGATTAGTCCCTGTGTTCATGTTGAG---TGGACCTGCAGACAGATGCC 432

Qy 254 -----SerGluArg 256

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Qy 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274

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QY 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
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; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
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; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-09-022-257-1
;
Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
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DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-022-257-1 (1-3288)
QY 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAAACCCTGACCCCGCTTCTCCCAAAAACATATATCAATCTTAGTTCTCTTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
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Db 433 AGCATCTGTACTCGAGGGTGCAGAGCTGTCCGTCTGAGCTGAACACCAATGAGCG 492
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 US-09-549-679-1
 ; Sequence 1, Application US/09549679
 ; Patent No. 6680057
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; Spriggs, Melanie
 ; Fanglow, William
 ; TITLE OF INVENTION: No. 6680057e1 Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/549,679
 ; FILING DATE: 14-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/620,694
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: USSN 08/410,535
 ; FILING DATE: 23 MARCH 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA
 / HYPOTHETICAL: NO
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 / ORIGINAL SOURCE:
 / ORGANISM: Mouse
 / STRAIN: HVS13 receptor
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 121..2715
 / SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-549-679-1

Alignment Scores:

Pred. No.: 1.5e-06 Length: 3288
 Score: 174.50 Matches: 119
 Percent Similarity: 31.6% Conservative: 65
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 Query Match: 4.8% Indels: 207
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US-10-719-202-2 (1-674) x US-09-549-679-1 (1-3288)

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: August 17, 2006, 09:11:08 ; Search time 269 Seconds
(without alignments)

6007.995 Million cell updates/sec

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Perfect score: 3605

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Published Applications NA_New:

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2339	64.9	2380	6	US-10-196-749-597
2	2339	64.9	2380	8	US-11-311-555-13
3	2339	64.9	2380	8	US-11-311-561-13
4	2339	64.9	2380	8	US-11-101-316-161
5	2339	64.9	2380	8	US-11-311-554-13
6	2339	64.9	2380	9	US-11-376-673-161
7	1971	54.7	2350	8	US-11-293-697-1517

ALIGNMENTS

RESULT 1

US-10-196-749-597
; Sequence 597, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24

Sequence 15241, A
Sequence 64946, A
Sequence 67778, A
Sequence 313, App
Sequence 218328,
Sequence 239031,
Sequence 233048,
Sequence 344477,
Sequence 233049,
Sequence 344478,
Sequence 361314,
Sequence 375554,
Sequence 446993,
Sequence 361313,
Sequence 387553,
Sequence 446992,
Sequence 403105,
Sequence 474151,
Sequence 261876,
Sequence 322393,
Sequence 361315,
Sequence 387555,
Sequence 446994,
Sequence 186516,
Sequence 364147,
Sequence 388229,
Sequence 447526,
Sequence 480243,
Sequence 6434, Ap
Sequence 364146,
Sequence 388228,
Sequence 447525,
Sequence 364072,
Sequence 447451,
Sequence 177972,
Sequence 62257, A
Sequence 42371, A
Sequence 13, Appl

1	PRIOR APPLICATION NUMBER: 60/063121
2	PRIOR FILING DATE: 1997-10-24
3	PRIOR APPLICATION NUMBER: 60/063486
4	PRIOR FILING DATE: 1997-10-21
5	PRIOR APPLICATION NUMBER: 60/063540
6	PRIOR FILING DATE: 1997-10-28
7	PRIOR APPLICATION NUMBER: 60/063541
8	PRIOR FILING DATE: 1997-10-28
9	PRIOR APPLICATION NUMBER: 60/063544
10	PRIOR FILING DATE: 1997-10-28
11	Prior Application data removed - See
12	NUMBER OF SEQ ID NOS: 612

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; SEQ ID NO 597
;
; LENGTH: 2380
;
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-597

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Alignment Scores:		
Pred. No.:	4,53e-171	2380
Score:	2339.00	459
Percent Similarity:	75.9%	Matches: 66
Best Local Similarity:	66.3%	Conservative: 133
Best Global Similarity:	64.9%	Mismatches: 34
Query Match:	6	Indels: 7
DB:		Gaps: 7

US-10-218-202-2 (1-674) x US-10-196-749-597 (1-2380)

QY	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
DB	233	ATGCTGTGCCCTGTTCTTGCTGTCTTGGCACTGGGCCGAAGCCAGTCGTCTCTCT	292
QY	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
DB	293	CTGAGAGGCTGTGGGCGCTCAGAGCGCTACCCACTCTCTCCGGGCTCTCTCTGCCG	352
QY	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
DB	353	CTCTGGGACAGTACATACTCTGCTGTCTGGGACATCGTGGCTGTCTCGGGCCCGTG	412
QY	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIysThrAspCys	80
DB	413	CTGGCGCTACGCACCTCGACAGAGCTGGTGTCTGAGGTGCCAAGAGAGACCCACTGT	472
QY	81	AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
DB	473	GACCTCTCTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGCACTGGGAGAGCCTGAA	532
QY	101	Glu-----AlaGlyIysSerAspSerGluLeuGlnGluSerArgAsnAlaSer	116
DB	533	GATGAGGAAGAAGTTTGGAGGACGCTGACTCAGGGGTGGAGAGCCTAGGAATGCCTCT	592
QY	117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTyProIleAlaArgCysAlaLeuLeu	136
DB	593	CTCCAGGCCAAGTCGTGTCTCTCTCCAGGCTACCCCTACTGCCCGCTCGTCTGCTG	652
QY	137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
DB	653	GAGGTGCAAGTGCCTGCTGCCCTTGTGCAAGTTTGGTTCAGTCTGTGGCTCTGTGGTATAT	712
QY	157	AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyThrIysProArg	176
DB	713	GACTGCTCGAGGCTCCCTAGGAGTAGGTTACGAATCTGGTCTTATCTACTCAGCCAGG	772
QY	177	TyrGlnIysGluLeuAsnLeuThrGlnLeuPro-----	188
DB	773	TACGAGAGGAATCTAACACACAGCAGCTGCTCCCTGCCCTGAGCTCAACGTGTCA	832
QY	189	---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPhe	207
DB	833	GCAGATGGTGACAACCTGCATCTGGTTCTGAATGTCTCTCAGAGAGCAGCACTTCGGCCTC	892
QY	209	LeuLeuSerLeuValProAsnAlaLeuValSerLeuTrpTrpValValAsnLeuThr	227

D89	TCCCTGTACTGGAATCAGGTCACGGGCCCCCCAAAACCCCGTGGGCACAAANAACCTGACT	952
QY	GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal	247
DB	953 GACACGCAAGATCATTAACCTTGAAACACACAGACCTGGTTCCCTGCTCTGTATTACAGGTG	1012
QY	TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly	267
DB	1013 TGGCCCTCTGGAACCTGACTCCGCTTAGGACGACAATCTGCCCTTCACGGAGACCCTCCGC	1072
QY	AlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln	287
DB	1073 GCACACCAAGAACCTCTGGCAAGCCGCCACCTGGACTGGACTGCTGACCTGCAGAGCTGGCTG	1132
QY	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpTrpGlnAlaProAspGln	307
DB	1133 CTGACGACACCGTCTGCTGCCGCCAAGAAGCGCACCTGCTGGCGGCTCCCGGGTGG	1192
QY	SerProCysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGluPro	327
DB	1193 GAACCCCTGCACGCACTGGTCCCACCGCTTCTCTGGGAGACGTCACCTGTGGACAGGTT	1252
QY	GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu	347
DB	1253 CTCGAGTCCCATTTGCTGAAGAGCCACCTAACCTCTGTGTTCAGTGAACAGCTCGAG	1312
QY	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet	367
DB	1313 AAGCTCAGCTGCAGAGTGCCTTGTGGCGTGACTCCCTGGGGCCCTCTCAAAGACGATGTG	1372
QY	LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer	387
DB	1373 CTAAGTGTGGAGACAGCGAGCCCGCCAGGACACAGATCCCTCTGTGCTTGGAAACCCAGT	1432
QY	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyCyluGluLeu	407
DB	1433 GGCTGTACTTCACTACCCAGCAAGAGCTCCACAGGGCAGCTCGCCTTGGAGAGTACTTA	1492
QY	LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySer	427
DB	1493 CTAACAGACTGCAGTCAAGCCAGTGTCTGCAGCTATGG--GACGATGACTTGGAGCG	1549
QY	LeuTrpAlaCysProMetAspLysIleHisArgArgTrpValLeuValTrpLeuAla	447
DB	1550 CTATGGCCCTGCCCATGGACAAATACATCCAACAGCGCTGGGCCCTCTGTGTGGTGGCC	1609
QY	CysLeuLeuLeuAlaAlaAlaPhePhePheLeuLeuLysLysAspArgArgLys	467
DB	1610 TGCCATACTCTTGGCGCTGGCGCTTCCTCATCTCTCTCAAAGAAGNTCAGCGAAA	1669
QY	-----AlaAlaArgGlySerArg	473
DB	1670 GGTGGCTGAGGCTCTTGAACAGGACGTCCTCGCTCGGGGGCGGCCGCAAGGGGC---CGC	1726
QY	ThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrluArgLeuValGlyAlaLeu	493
DB	1727 CGCGCTCTGCTCTCTACTCAGCCGATGACTCGGGGTTTCGAGCGCCTTGTGTGGCGCCCTG	1786
QY	AlaSerAlaLeuSerGlnMetProLeuArgValAlaValaAspLeuTrpSerArgArgGlu	513
DB	1787 GCGTCGGCCCTGTCCAGTGCCTCGCTGGCGTGGCCGTAGACCTGTGGAGCCGCTCGTGA	1846
QY	LeuSerAlaHisGlyAlaLeuAlaTrpPheHisIleGlnArgArgArgIleLeuGlnGlu	533
DB	1847 CTGAGCGCGAGGGGCCCGTGGCTTGTGTTTCACGCGCAGCGGGGCCAGACCTTCAGAG	1906
QY	GlyGlyValValIleLeuLeuPhePheSerProAlaAlaValaGlnCysGlnGlnTrpLeu	553
DB	1907 GCGCGCGTGGTGGTCTTCTCTTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTA	1966
QY	GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu	570

Db 233 ATGCCTGTGCCTGGTCTTCTGCTGCTGGCACTGGGCGGAGCCCGAGTGGTCTTCT 292
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 293 CTGGAGAGCTTGTGGGGCTCAGAGCGTACCACCTGCTCTCCGGGCTCTCTCTGGCG 352
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuSerAlaProGlyProVal 60
Db 353 CTCTGGGACAGTACATCTCTGCTGCTGGGACATCGTGCCTCGGGCCCGGTG 412
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 413 CTGGCGCTTACGACCTGCACAGAGCTGTGTGCTGAGGTGCCAGAGGAGCGACTGT 472
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 473 GACCTCTGTCTGCTGTGGCTGTCTCATCTTGCCCTGTGANTGGGCACTGGGAGAGCCCTGAA 532
Qy 101 Glu-----AlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSer 116
Db 533 GATGAGGAGAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGAGCCCTAGGAATGCCTCT 592
Qy 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProLleAlaArgCysAlaLeuLeu 136
Db 593 CTCCAGGCCCAAGTCTGCTCTCTCCCTCCAGGCCCTACCTCTACTGCGCGCTGCTCTGCTG 652
Qy 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156
Db 653 GAGTGTCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Qy 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnLileTrpSerTyrThrLeuProArg 176
Db 713 GACTGCTTCGAGGCTGCCCTAGGAGTGAGTACGAACTGTCTCTATATCTACGCCCCAGG 772
Qy 177 TyrGlnLysGluLeuAsnLeuThrGlnLeuPro----- 188
Db 773 TACGAGGAAGAACTCAACACACACAGCAGCTGCTGCCCTCGCCCTCGCTCAACGTGTCA 832
Qy 189 ---AspGlyAspAsnValLeuThrLeuAspValSerGluGluGlnAspPheSerPhe 207
Db 833 GCAGATGGTGACACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
Qy 208 LeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThr 227
Db 893 TCCCTGTACTGGAATCAGTTCAGGGCCCCCAAAACCCCGTGGCACAAACCTGACT 952
Qy 228 GlyProGlnAsnLileThrLeuAsnHisThrAspLeuValProCysLysLileGlnVal 247
Db 953 GGACCGCAGATCAATTACCTTGAACACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
Qy 248 TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly 267
Db 1013 TGGCCTCTGGAACCTGACTCGTTAGACGCAACATCTGCCCTTTCAGGGAGGAGCCCGCG 1072
Qy 268 AlaHisArgAsnLeuTrpHisLileAlaArgLeuArgValLeuSerProGlyValTrpGln 287
Db 1073 GCACACAGAACCTCTGGCAAGCCCGCGACTGCGACTGTGCTGACCTCGCAGAGCTGCTG 1132
Qy 288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln 307
Db 1133 CTGGACGACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
Qy 308 SerProCysGlnProLeuValProValProGlnLysAsnAlaThrValAsnGluPro 327
Db 1193 GACCCCTCGCCAGCCACTGGTCCCAACCGCTTCTTGGGAGAACGCTGCTGGGCAAGGTT 1252
Qy 328 GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerTrpGlu 347
Db 1253 CTGAGTGTCCATGTGTGAAGGCGCACCTTAACCTCTGTGTTCAGGTGAACAGCTCGGAG 1312
Qy 348 LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet 367
Db 1313 AAGCTGCAGCTGCAGGAGTGTCTGTGGCTGACTCTCCCTGGGGCTCTCTCAAGAGCATGTG 1372

Qy 368 LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer 387
Db 1373 CTACTGTGGAGACAGAGCCCGCCAGGACACAGATCCCTCTGTGCTTGGACCCAGT 1432
Qy 388 GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu 407
Db 1433 GGCTGTACTTCACTTACCAGCAAGCCCTCCACGAGGCGAGCTCGCTTGGAGACTACTTA 1492
Qy 408 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySer 427
Db 1493 CTACAAGACCTGCAGTCAGCCAGTGTCTGAGCTATGG---GACGATGACTTCTGGAGCG 1549
Qy 428 LeuTrpAlaCysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAla 447
Db 1550 CTATGGGCTTCCCTCAGGACAAATACATCCACAGGCTTGGGCTCTGTGTGGCTGGCC 1609
Qy 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLysLysAspArgArgLys 467
Db 1610 TGCTACTCTTTCGCGCTGCTTTCCTCTCATCTCTCTCAAAAAGGATCACCGCAAA 1669
Qy 468 -----AlaAlaArgGlySerArg 473
Db 1670 GGTGCTGAGGCTTGTAAACAGGACGTCCTCGGGGGCGCGCCGAGGGC---CGC 1726
Qy 474 ThrAlaLeuLeuLeuHisSerAlaAspGlyTyrGluArgLeuValGlyAlaLeu 493
Db 1727 CGGCTCTGTCTCTTACTCAGCGGATGACTCGGGTTTCAGAGGCTTGTGGGCGCTCTG 1786
Qy 494 AlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgLys 513
Db 1787 GCGTGGGCTGTGCCAGCTGCGCTGCGGTGCGGTAGACCTGTGAGCGCTGTGNA 1846
Qy 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgLileLeuGlnGlu 533
Db 1847 CTGAGCGCGAGGGCGGCTGTGGTGTGTTTTCAGCGCAGCGCGCCAGACCTGSCAGGAG 1906
Qy 534 GlyGlyValValLileLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
Db 1907 GCGCGGTGTGTGTCTTCTCTCTCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 1966
Qy 554 GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaTrpLeu 570
Db 1967 CAGGATGGGTGTTCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCTTCGCGCGCTCGCTC 2026
Qy 571 SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyr 590
Db 2027 AGCTGTGCTGTGCGCGACTTCTTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCTGCG 2086
Qy 591 PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe 610
Db 2087 TCGACAGGCTGTCTCACCGGAGCGGTACCGCTTTCGCGCGCGCGCGCGCGCGCTTTC 2146
Qy 611 SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer 630
Db 2147 ACATGCGCTCCCACTGCGCAGACTTCTTGGGGGCGCTGCGAGCAGCTCGCGCGCGCT 2206
Qy 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 2207 TCCGGGCGGTCTCAAGAGAGAGGAGCAAGTGTCCCGGGCGCTTTCAGCAGCGCGCTGAT 2266
Qy 651 SerCys-----ThrSerSerGluAlaProGly 660
Db 2267 AGTACTTCCATCCCGGGGACTTCCCGCGCGCGGGA 2302

RESULT 4

US-11-101-316-161
; Sequence 161, Application US/1101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
 ; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
 ; FILE REFERENCE: P3230R1C17C1
 ; CURRENT APPLICATION NUMBER: US/11/101,316
 ; CURRENT FILING DATE: 2005-04-06
 ; PRIOR APPLICATION NUMBER: 10/063526
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 09/380137
 ; PRIOR FILING DATE: 1999-08-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 161
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-11-101-316-161

Alignment Scores:
 Pred. No.: 4,53e-171 Length: 2380
 Score: 2339, 00 Matches: 459
 Percent Similarity: 75.9% Conservative: 66
 Best Local Similarity: 66.3% Mismatches: 133
 Query Match: 64.9% Indels: 34
 Gaps: 7
 DB:

US-10-719-202-2 (1-674) x US-11-101-316-161 (1-2380)
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 DB 233 ATGCGTGTGCCGTGGTCTTCTGCTGCTTGGCATCTGGCCGAGCCAGTGGTCTTCT 292
 QY 21 LeuGluArgLeuMetGluProGlnAaspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 DB 293 CTGGAGAGCGTGTGGGGCCCTCAGGACGCTACCCCACTGCTCTCGGGGCTCTCTCGCGCG 352
 QY 41 LeuTrpAaspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 DB 353 CTCCTGGACAGTGACATATCTGCTGCTGCTGGGACATCTGCTGCTGGGCGCTCTCGCGCG 412
 QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAaspCys 80
 DB 413 CTGGCGCCCTACGCACCTGCAGACAGAGCTGGTGTGCTGAGGTGCCAGAGAGACCGACTGT 472
 QY 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 DB 473 GACCTCTGTCTGCTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAA 532
 QY 101 Glu-----AlaGlyLysSerAaspSerGluLeuGlnGluSerArgAasnAlaSer 116
 DB 533 GATGAGGAAAGTTTGGAGAGAGCAGCTGACTCAGGGGTGGAGAGCCTAGGAATGCCTCT 592
 QY 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrrProIleAlaArgCysAlaLeuLeu 136
 DB 593 CTCAGGCCCAAGTGTGCTGCTCTCTCCAGGCCCTACCTTACTGCGCGCTGCGCTGCTGCTG 652
 QY 137 GluValGlnValProAlaAaspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156
 DB 653 GAGGTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
 QY 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrrThrLysProArg 176
 DB 713 GACTGCTCAGGCTGCGCTAGGAGTGTAGGATCGAATCTGGTCTCTATCTACTCAGCCAGG 772
 QY 177 TyrGlnLysGluLeuAenLeuThrGlnGlnPro----- 188

773 TACGAGAAAGGAACTCAACCAACACACAGCAGCTGCGCTGCGCTGCGCTCAACGTGTCA 832
 QY 189 ---AspGlyAaspAenValLeuLeuThrLeuAaspValSerGluGluGlnAaspSerPhe 207
 DB 833 GCAGATGGTGCACACAGTGCATCTGGTGTGAATGTCTCTGAGGAGCAGCAGCTTCGGCCTC 892
 QY 208 LeuLeuTyrrLeuArgProValProAaspAlaLeuLysSerLeuTrpTyrrLysAenLeuThr 227
 DB 893 TCCTGTACTTGAATCAGGTCCAGGGCCCCCAAAACCCCGGTGGCAGCAAAAACCTGACT 952
 QY 228 GlyProGlnAenIleThrLeuAenHisThrAaspLeuValProCysLeuCysIleGlnVal 247
 DB 953 GGACCGCAGATCATTAACCTTGAACCAACAGACAGCTGTTCCCTGCTCTGTATTTCAGGTG 1012
 QY 248 TrpSerLeuGluProAaspSerGluArgValGluPheCysProPheArgGluAaspProGly 267
 DB 1013 TGGCTCTGGACACTGACTCGGTAGGACGAACATCTGCCCTTTCAGGGAGGAGCCCCCGC 1072
 QY 268 AlaHisArgAenLeuTrpHisIleAlaArgLeuArgValLeuTrpGln 287
 DB 1073 GCACACAGAACTCTGCGAAGCGCCGACTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1132
 QY 288 LeuAaspAlaProCysCysLeuProGlyLysValThrLeuCysTrpTrpGlnAlaProAaspGln 307
 DB 1133 CTGGACGACCGTGTCTGCTGCCGAGACGGCGCACTGTGCTGCGGGCTCCGGGTGGG 1192
 QY 308 SerProCysGlnProLeuValProValProGlnLysAenAlaThrValAasnGluPro 327
 DB 1193 GACCCCTGCCAGCACTGGTCCACCGCTTTCCTGGGAGAACGTCACCTGTGGACCAAGTT 1252
 QY 328 GlnAaspPheGlnLeuValAlaGlyHisProAenLeuCysValGlnValSerThrTrpGlu 347
 DB 1253 CTCGAGTTCCCATTTGCTGAAAAGGCCACCCCTAACCTCTGTGTTCAGGTGAACAGCTCGGAG 1312
 QY 348 LysValGlnLeuGlnAlaCysSerTrpAlaAaspSerLeuGlyProPheLysAaspAaspMet 367
 DB 1313 AAGCTGACGCTGCAGAGTGTGTTGGTGTGACTCCCTGGGGGCTCTCAAAAGACGATGTG 1372
 QY 368 LeuLeuValGluMetLysThrGlyLeuAenAenThrSerValCysAlaLeuGluProSer 387
 DB 1373 CTACTGTTGAGACACAGAGGCCCCCGAGGACAAACAGATCCCTCTGTCCTTGGACCCAGT 1432
 QY 388 GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaAargLeuGlyGluLeu 407
 DB 1433 GGTGTACTTCTACTCCAGCAAGGCCCTCCAGGGGAGCTCGCTTGGAGAGTACTTA 1492
 QY 408 LeuGlnAaspPheArgSerHisGlnCysMetGlnLeuTrpAasnAaspAasnMetGlySer 427
 DB 1493 CTACAAGACCTGCAGTCAGGCCAGTCTCTGCACTATGG---GACGATGACTTTGGAGCGC 1549
 QY 428 LeuTrpAlaCysProMetAaspLysTyrrIleHisArgArgTrpValLeuValTrpLeuAla 447
 DB 1550 CTATGGGCTGCGCCCATGGACAATACATCCACAGCGCTGGGCCCTCTGCTGTGGCTGGCC 1609
 QY 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLysLysLysAaspArgArgLys 467
 DB 1610 TGCTACTCTTTGCGCGTGGCTTTCCTCATCTCTCTTCAAAAAGGATACACGGAGAA 1669
 QY 468 -----AlaAlaArgLysSerArg 473
 DB 1670 GGGTGGCTGAGGCTTTGAAACAGAGCGTCCGCTCGGGGGCGCGCCGAGGGGCG---CGC 1726
 QY 474 ThrAlaLeuLeuLeuHisSerAlaAaspGlyAlaGlyTyrrGluArgLeuValGlyAlaLeu 493
 DB 1727 GCGGCTCTGTCTCTCTACTCAGCCGATGACTCGGGTTTCAGGCGCTTGGTGGCGCGCCCTG 1786
 QY 494 AlaSerAlaLeuSerGlnMetProLeuArgValAlaValAaspLeuTrpSerArgArgGlu 513
 DB 1787 GCGTGGCGCTGTGCCAGCTGCCCTGCGGTGGCCGTAGACCTGTGGAGCCGCTGCTGAA 1846
 QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgArgIleLeuGlnGlu 533

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Db 1847 CTGAGCGCGCAGGGGCGCGTGGTCTTTCACGCGCAGCGCGCCACAGACCCCTGCGAGGAG 1906
Qy 534 GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
Db 1907 GCGCGCGTGGTGTCTTCTCTCCCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1966
Qy 554 GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaIleTrpLeu 570
Db 1967 CAGGATGGGTGTCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 2026
Qy 571 SerCysValLeuProAspPheLeuGlnGlnArgAlaThrGlyArgTrpValGlyValTrp 590
Db 2027 AGTTCGCGTGTCCCGACTTCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGC 2086
Qy 591 PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe 610
Db 2087 TTCGACAGGCTGTCCACCGCGGAGCGGTACCGCGCTTTTCGCGCGCGCGCGCGCTTC 2146
Qy 611 SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer 630
Db 2147 ACATGCGCTCCCACTGCGCAGACTTCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGGT 2206
Qy 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 2207 TCCGCGCGGTCCCAAGAGAGAGCGGAGCAAGTGTCCCGGCGCGCTTCAGCGCGCGCTGGAT 2266
Qy 651 SerCys-----ThrSerSerSerGluAlaProGly 660
Db 2267 AGCTACTTCCATCCCCCGGGGACTTCCGCGCGCGGGA 2302

RESULT 5
US-11-311-554-13
; Sequence 13, Application US/11311554
; Publication No. US20060134755A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/11/311,554
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 13
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-311-554-13

Alignment Scores:
Pred. No.: 4,53e-171 Length: 2380
Score: 2339.00 Matches: 459
Percent Similarity: 75.9% Conservative: 66
Best Local Similarity: 66.3% Mismatches: 133
Query Match: 64.9% Indels: 34
DB: 8 Gaps: 7

US-10-719-202-2 (1-674) x US-11-311-554-13 (1-2380)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 233 ATGCCTGTGCTCCCTGGTCTTGTCTCTTGGCACTGGCGCGAAGCCAGCGTGGTCTTCT 292
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 293 CTGGAGAGCTGTGGGGCTCAGGACGCTACCCACTGTCTCTCGGGGCTCTCTCTGCGC 352
Qy 41 LeuTrpAspGlyValValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 353 CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGTCTCTCGGGCCCGGTG 412
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 413 CTGGCGCTTACCACCTGCAGACAGAGCTGGTGTGCTGAGGTGCGCAGAGGAGACCGACTGT 472
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 473 GACCTCTGTCTGGGTGTGGTGTCTTCCACTTGGCGGTGCTGAGGTGCGCAGAGGAGACCTGAA 532
Qy 101 Glu-----AlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSer 116
Db 533 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCTAGGAATGCTCT 592
Qy 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrrProIleAlaArgCysAlaLeuLeu 136
Db 593 CTCCAGGCCCAAGTCGTGCTCTCTTCCAGGCTTACCTTACTGCGCGCTGCGTCTGCTG 652
Qy 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156
Db 653 GAGGTGCAAGTGTCTGCTGCTGCTTGTGCAAGTGTGTCAGTCTGTGGGCTCTGTGGTATAT 712
Qy 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArg 176
Db 713 GACTGTCTCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772
Qy 177 TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro----- 188
Db 773 TAGGAGAGGAAGTCAACACACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832
Qy 189 ---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnGlnAspPheSerPhe 207
Db 833 GCAGATGGTGACAACTGATCTGTTCTGAATGTCTGAGGAGCAGACACTTCGGGCTC 892
Qy 208 LeuLeuTyrrLeuArgProValProAspAlaLeuLysSerLeuTrpTrpLysAsnLeuThr 227
Db 893 TCCCTGTACTGGNATCAGGTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTACT 952
Qy 228 GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal 247
Db 953 GGACCGCAGATCATTTACCTTGAACCAACACAGACCTGTTCCCTGCTCTGTATTTCAGGTG 1012
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QY 248 TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly 267
 Db 1013 TGGCTCTGGAAACCTGACTCGTTAGGACGAACATCTGCCCTTCAGGAGGACCCCGC 1072
 QY 268 AlaHisArgenLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287
 Db 1073 GCACACAGAACCTCTGCGAAGCCCGGACTGCGACTGCTGACCTCGCAGCTGGCTG 1132
 QY 288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln 307
 Db 1133 CTGACGACCGCTGCTGCTGCCCGCAGAACGGCACTGTGCTGCGCGGCTCGGGTGG 1192
 QY 308 SerProCysGlnProLeuValProValProGlnLysAsnAlaThrValAsnGluPro 327
 Db 1193 GACCCCTGCCAGCCACTGGTCCACCGCTTTCTCGGGAGAACGTCATCTGGACAGGTT 1252
 QY 328 GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 347
 Db 1253 CTCGAGTTCCTATGCTGAAGGCCACCTTAACCTCTGTGTTCAAGTGAACAGCTCGGAG 1312
 QY 348 LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMet 367
 Db 1313 AAGCTGCACTGCAAGAGTGTGTGGCTGACTCCCTGGGGCCCTCTCAAAAGAGATGTG 1372
 QY 368 LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer 387
 Db 1373 CTACTGTTGGAGACAGAGCCCGCCAGCAACAGATCCCTGTGCTTGAACCCAGT 1432
 QY 388 GlyCysThrProLeuProSerMetAlaSerThrAlaAlaArgLeuGlyGluLeu 407
 Db 1433 GGCTGTACTTACTACCCAGCAAGCCCTCCAGAGCGAGCTCGCTTGGAGTACTTA 1492
 QY 408 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspMetGlySer 427
 Db 1493 CTACAAGACTGCACTGAGCCAGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
 QY 428 LeuTrpAlaCysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAla 447
 Db 1550 CTATGGGCTGCCCATGACAAATACATCCACAGCGCTGGGCTGCTGCTGCTGCTGCTG 1609
 QY 448 CysLeuLeuAlaAlaLeuPhePhePheLeuLeuLysLysAspArgLys 467
 Db 1610 TGCGTACTCTTTCGCTGCTGCTTCCCTCATCTCTTCTCAAAAGGATACCGGAA 1669
 QY 468 -----AlaAlaArgGlySerArg 473
 Db 1670 GGGTGGCTGAGGCTCTTGAACAGGAGCTCGCTCGGGGGCGCCGCGAGGCGC---CGC 1726
 QY 474 ThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeu 493
 Db 1727 GCGCTCTGCTCTACTCAGCGGATGACTCGGGTTTCAGCGCTGCTGGGCGGCTGCTG 1786
 QY 494 AlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGlu 513
 Db 1787 GCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1846
 QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgArgIleLeuGlnGlu 533
 Db 1847 CTGAGCGCGAGGGCCCGTGGCTTGTTCACGCGCAGCGCGGCGCAGACCTCGCAGGAG 1906
 QY 534 GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
 Db 1907 GCGGCGTGGTGGTCTTCT 1966
 QY 554 GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu 570
 Db 1967 CAGATGGGGTGTCCGGCCCGGGCGCAGCGCCCGCAGCAGCGCTTCCGCGCTCGCTC 2026
 QY 571 SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTyr 590
 Db 2027 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2086
 QY 591 PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe 610

Db 2087 TTTCGACAGGCTCTCCACCGGACCGGTACCGCCCTTTTCCGACCGTGCCTCTTC 2146
 QY 611 SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer 630
 Db 2147 ACATGCTCTCCCACTTCCGACTTCTTGGGGCCCTTGCAGCAGCTCGCGCCGCT 2206
 QY 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
 Db 2207 TCCGGCGGCTCTCAAGAGAGAGCGGAGCAAGTGTCCGGGGCCCTTCAGCAGCCCTGGAT 2266
 QY 651 SerCys-----ThrSerSerGluAlaProGly 660
 Db 2267 AGCTACTTTCATCCCGGGGACTCCCGCGCCGGA 2302
 RESULT 6
 US-11-376-673-161
 ; Sequence 161, Application US/11376673
 ; Publication No. US20060160186A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
 ; TITLE OF INVENTION: LUNG TUMOR
 ; FILE REFERENCE: P3230R1C165C
 ; CURRENT APPLICATION NUMBER: US/11/376,673
 ; CURRENT FILING DATE: 2006-03-14
 ; PRIOR APPLICATION NUMBER: 10/063742
 ; PRIOR FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 60/170262
 ; PRIOR FILING DATE: 1999-12-09
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 161
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-11-376-673-161
 Alignment Scores:
 Pred. No.: 4,53e-171 Length: 2380
 Score: 2339.00 Matches: 459
 Percent Similarity: 75.9% Conservative: 66
 Best Local Similarity: 66.3% Mismatches: 133
 Query Match: 64.9% Indels: 34
 DB: 9 Gaps: 7
 US-10-719-202-2 (1-674) x US-11-376-673-161 (1-2380)
 QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
 Db 233 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
 QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 293 CTGGAGAGCTGTGTGGGGCTTCAGGACGCTACCCACTGCTCTCCGGGCTCTCTCTGCGC 352
 QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 353 CTCTGGAGCAGTGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
 QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 413 CTGGCGCTACGCACTTCGACAGCAGAGTGTGTGAGTGTGACAGGAGGACCGACTGT 472
 QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100

D	b		473	GACCTCTGTCGTGGTGGCTGTGCCACTTGCCCGCTGCATGGGCACTCGGGAAGAGCCTGAA	532
Q	y		101	Glu-----AlaGlyIysSerAspSerLeuGlnGluSerArgAsnAlaSer	116
D	b		533	GATCAGGAAGAATTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCCTAGGAATGCCTCT	592
Q	y		117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrrProIleAlaArgCysAlaLeuLeu	136
D	b		593	CTCAGGCCCCAAGTCGTCTCTCCCTCCAGGCTACCCTACTAGTCCCGCTGCCTCTGCTG	652
Q	y		137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
D	b		653	GAGGTGCAGTGCCTGCTGCCCTTTGTGAGTTGGTCAGTCTGTGGGCTCTGTGGTATAT	712
Q	y		157	AspCysPheGlnAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrrThrLysProArg	176
D	b		713	GACTGCTTCGAGGCTGCCCTAGGAGGTAGGTACGAATCTGGTCTCTATACTCAGCCCAGG	772
Q	y		177	TyrGlnIysGluLeuAsnLeuThrGlnGlnLeuPro-----	188
D	b		773	TACGAGAAGGAACCTCAACACACACAGCAGCTGCCTGCCCTTGGCTCAACGTGTCA	832
Q	y		189	--AspGlyAspAsnValLeuThrLeuAspValSerGluGluGlnAspPheSerPhe	207
D	b		833	GCAGATGGTGACAACAGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTC	892
Q	y		208	LeuLeuTyrrLeuArgProValProAspAlaLeuLysSerLeuTyrrLyrsAsnLeuThr	227
D	b		893	TCCCTGTACTGGAATCAGTCCAGGGCCCCCAAACCCCGGTGGCACAAAACCTGACT	952
Q	y		228	GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal	247
D	b		953	GGACCGCAGATCATTTAGCTTGAACACACACAGACCTGGTTCCCTGCCCTCTGTATTCA	1012
Q	y		248	TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly	267
D	b		1013	TGGCCTCTGGAACCTGACTCCGTTAGGAGCAACATCTGCCCTTCAGGAGAGACCCCGC	1072
Q	y		268	AlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln	287
D	b		1073	GCACACAGAACCTCTGGCAAGCCGCCGACTGCGACTGTGTAACCTTCAGAGCTGGCTG	1132
Q	y		288	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln	307
D	b		1133	CTGAGCACAACGCTCGCTCGCTCCCGCAGAAAGCGCACTGTGTGGCGGCTCCGGGTGG	1192
Q	y		308	SerProCysGlnProLeuValProProValProGlnIlysAsnAlaThrValAsnGluPro	327
D	b		1193	GACCCCTGCCACGACACTGGTGTCCACCCGCTTCTCTGGGAGAACGTCATCTGGGACGG	1252
Q	y		328	GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu	347
D	b		1253	CTCGAGTTCCTGCTGAAAGGCCACCTTAACCTCTGTGTTCAAGGTGAACAGCTCGGAG	1312
Q	y		348	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet	367
D	b		1313	AAGCTGAGCTGCAGGAGTGCTTGTGGCTGACTCCCTGGGGCTCTCCAAGACGATGTG	1372
Q	y		368	LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer	387
D	b		1373	CTACTGTTGGAGACACGAGGCCCCACGAGCAACAGATCCCTCTGTGCTTGGAAACCCAG	1432
Q	y		388	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu	407
D	b		1433	GGCTGTACTTCACTACCCAGCAAGCTTCCACGAGGGCAGCTGCCCTTGAGAGTAGTCTTA	1492
Q	y		408	LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySer	427
D	b		1493	CTACAAGACCTGCAGTCAGGCCAGTGTGCAGCTATGG--GACGATGACTTGGGAGCG	1549
Q	y		428	LeuTrpAlaCysProMetAspLysTyrrIleHisArgArgTrpValLeuValTrpLeuAla	447
D	b		1550	CTATGGCCCTGCCCAATGGAACAATACTCAACAAGCGCTGGGCCCTCTGTGTGCTGGCC	1609

Qy	448	CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys	467
Db	1610	TGCCTACTCTTTGGCGGTGGCTTTCCTCATCTCCTTCATAAAAGGATCACGCGAAA	1669
Qy	468	-----AlaAlaArgGlySerArg	473
Db	1670	GGTGCGCTGAGGCTTTGAAACAGGACGTCCGTGGGGGGCGGCCGACGGGGC---CGC	1726
Qy	474	ThrAlaLeuLeuHisSerAlaAspGlyValaGlyTyrGluArgLeuValGlyValaLeu	493
Db	1727	GCGGCTCTGCTCTCTACTCAGCGAGTACTCGGGTTTCAGGCGCCTGTGTGGGCGCCCTG	1786
Qy	494	AlaSerAlaLeuSerGlnMetProLeuArgValaValaValaAspLeuTrpSerArgArgGlu	513
Db	1787	GCGTCGGCCTGTGCCAGCTGCGCTGCGCGTGGCCGTAGACCTGTGGAGCGCGTCGTGA	1846
Qy	514	LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgArgIleLeuGlnGlu	533
Db	1847	CTGAGCGCAGGGGCGCGTGGCTGTGGTTTTCAAGCGAGCGGCGCCACAGACCTTCAGGAG	1906
Qy	534	GlyGlyValValIleLeuLeuPheSerProAlaAlaValaGlnCysGlnGlnTrpLeu	553
Db	1907	GCGCGCGTGGTGGTCTTCTCTCCCGTGGGTGGCGCTGTGCAGCGAGTGGCTA	1966
Qy	554	GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu	570
Db	1967	CAGGATGGGTGTCCGGGCCCGGGCGCACGGCCCGCACGACGCTTCCGCGCCTCGCTC	2026
Qy	571	SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyr	590
Db	2027	AGCTGCGTGTGCCCGACTTCTTTCAGGCGCGGCGCGCCGCGCAGTACGTGGGGGGCCCTGC	2086
Qy	591	PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe	610
Db	2087	TTTCACAGGTGTCTCCACCAGAGCGCGTACC CGCCCTTTTCGCAACCGTGC CGCTTC	2146
Qy	611	SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSer	630
Db	2147	ACATCGCTCCCMACCTGCCAGACTTCTGGGGGGCCCTGCAGAGCCTCGCGCCCGCGT	2206
Qy	631	AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp	650
Db	2207	TCCGGGCGGTCCAAGAGAGAGCGGCAAGTGTCCGGGCGCCTTCAGCAGCCCTGGAT	2266
Qy	651	SerCys-----ThrSerSerSerGluAlaProGly	660
Db	2267	AGCTACTTTCATCCCCCGGGGATCTCCCGCCCGGGA	2302

RESULT 7

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US-11-293-697-1517
; Sequence 1517, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1517
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1517

Alignment Scores:
Pred. No.: 1,25e-142 Length: 2350
Score: 1971.00 Matches: 413
Percent Similarity: 62.7% Conservative: 59

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Tue Aug 22 11:34:36 2006

Best Local Similarity:	54.8%	Mismatches:	125
Query Match:	54.7%	Indels:	157
DB:	8	Gaps:	11
US-10-719-202-2 (1-674) x US-11-293-697-1517 (1-2350)			
QY	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer	20
DB	209	ATGCTGTGCGCTGGTCTTCTGCTTGGCACTGGGGCGGAAGCCAGTGGTCTTCT	268
QY	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
DB	269	CTGGAGAGCTTGTGGGGCTTCAGAGAGCTTACCCACTGCTCTCCGGGCTCTCTGCGC	328
QY	41	LeuTrpAsp-----	43
DB	329	CTCTGGGG-TGCCACCAAAATCTGGGCTTGGAAACAGCTTCAGCTCCACCGCTCTCTCA	387
QY	44	-----GlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
DB	388	CACACAGACAGTGCATACTCTGCTGCTGGCTGGGACATCGTGCCTGCTCCGGGCCCCGTG	447
QY	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
DB	448	CTGGCGCCCTACGACCTGCAGACAGCTGGTGTGCTGAGTGCAGAGAGAGACTGACTGT	507
QY	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
DB	508	GACCTCTGCTGGCTGTGGCTGTCTCACTTGGCGGTGATGGGACATGGGAAGAGCTGAA	567
QY	101	Glu-----AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer	116
DB	568	GATGAGAAAAGTTTGGAGAGCAGCTGACTTGGGGTGGAGAGCTTAGGAATGCTCT	627
QY	117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrrProIleAlaArgCysAlaLeuLeu	136
DB	628	CTCAGGCCCAAGTGTGCTCTCTCTCCAGGCTTACCTACTGCCCGCTGGCTGCTGCTG	687
QY	137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
DB	688	GAGGTGAAGTGTCTGCTGCCCTTGTGCAGTTGGTCAAGTCTGTGGCTCTGTGGTATAT	747
QY	157	AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrrLysProArg	176
DB	748	GACTGTCTGAGGCTGCCCTAGGAGTGGATGAGTACGAATCTGGTCTTATCTCAGCCAGG	807
QY	177	TyrGlnLysGluLeuAsnLeuThrGlnLeuPro-----	188
DB	808	TACGAGAAGGAACCTCAACACACAGCAGCTGCTGCCCTGCCCTCAAGGTGCA	867
QY	189	---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe	207
DB	868	GCAGATGGTGACAACGTCACTGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTC	927
QY	208	LeuLeuTyrrLeuArgProValProAspAlaLeuLysSerLeuTyrrLysAsn-----	225
DB	928	TCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAACCCCGGTGGCACAACCTGTGTG	987
QY	225	-----	225
DB	988	AGGCTCTCCCTTCCCAAGTCCATTCCTACTGTAGGCGGATGCTGTGCAAGAGCAGAG	1047
QY	226	-----LeuThrGly	228
DB	1048	TGCCATATCAGAGAGGATCTTTGAAGAGAGCTCACCCACAGCAAGGAAAATTGACTGA	1107
QY	229	ProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrp	248
DB	1108	CCGAGATATTAACCTTGAACACACAGACCTGTTCCCTGCTCTGTATTACAGTGTGG	1167
QY	249	SerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAla	268
DB	1168	CCTCTGGAACTGACTCCGTAGGACGAACATCTGCCCTTTCAGGAGGAGACCCCCGCA	1227
QY	269	HisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeu	288
DB	1228	CACCAGAACCTCTGGCAAGCCGCCGACTGTGAGTGTCTGAGTGTGAGCTGGCTGTG	1287
QY	289	AspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSer	308
DB	1288	GAGCAGACCGTGTCTGCTGCCGAGAGCGGCACTGTGTGGCGGCTCCCGGTGGGAC	1347
QY	309	ProCysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGln	328
DB	1348	CCCTGCCAGCCTGCTCCACCGCTTCTCTGGGAGAACGTCACCTGTGTGACAGGTTC	1407
QY	329	AspPheGlnLeuValAlaGlyHisProAsnLeuCysVal---GlnValSerThrTrpGlu	347
DB	1408	GAGTTCCCAATTCGTGAAGGCCACCTTACCTCTGTTCAGCAGGTGAACAGCTCGGAG	1467
QY	348	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet	367
DB	1468	AGCTCAGCTGCAGAGTGTGTGG-----	1494
QY	368	LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer	387
DB	1494	-----	1494
QY	388	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu	407
DB	1494	-----	1494
QY	408	LeuGlnAspPheArgSerHisGlnCysMetGln-LeuTrpAsnAspAspAsnMetGlyse	427
DB	1495	-----GCTGCTATGG---GACGATGACTTGGAGC	1521
QY	427	rLeuTrpAlaCysProMetAspLysTyrrIleHisArgArgTrpValLeuValTrpLeuAl	447
DB	1522	GCTATGGGCTTGGCCCATGTGACAAATACATCCACAGCGCTGGGCTCTGTGTGGCTGC	1581
QY	447	aCysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLysLysAspArgArgLy	467
DB	1582	CTGCTACTCTTTCGCTGCTCTTCTCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT	1641
QY	467	-----AlaAlaArgGlySerAr	473
DB	1642	AGGGTGGCTGAGGCTCTTGAACAGGAGCTCCGCTCGGGGGCGGCCGCGAGGGGC---	1698
QY	473	gThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrrGluArgLeuValGlyAlaLe	493
DB	1699	CGCGCTCTGCTCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCTGTGTGGCGCCT	1758
QY	493	uAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGly	513
DB	1759	GGCGTGGGCTGTGCCAGCTCCCGCTGGCGGTGGCGGTAGACCTGTGGAGCCGCTGTA	1818
QY	513	uLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgGileLeuGlnG	533
DB	1819	ACTGAGCGCGAGGGCGCGTGTGTGTTCACGCGCAGCGCGGCCGACACCTCGAGGA	1878
QY	533	uGlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnTrpLe	553
DB	1879	GGCGCGGTGGTGTGTCTCTCTCTCCCGTGGGTGGCGCTGTGCGAGGAGTGGCT	1938
QY	553	uGlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaTrpLe	570
DB	1939	ACAGGATGGGTGTCCGGGCGCGGCGCGCACCGCCGACGCTTCGCGGCTCGCT	1998
QY	570	uSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrrValGlyValTy	590
DB	1999	CAGTGTGGTGTGCCGACTTCTTGAGGGCGCGGGCGCGCGGCGAGCTACGTGGGGCGCTG	2058
QY	590	rPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPh	610
DB	2059	CTTCGACAGGCTGTCTCCACCGCGAGCGCTACCGCCCTTTCGCGCACCGGTGCCGCTT	2118


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411 heArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaC 431
125 -----CTATGG-----GACGATGACTTGGGAGCGCTATGGGCGCT 92
431 ysProMetAspLysTyrIleHisArgTrpValLeuValTrpLeuAlaCysLeuLeuL 451
91 GCGCCATGGACAAATACATCCACAGCGCTGGGCCCTCGTGTGGCTGGCGCTACTCT 32
451 euAlaAlaLeuPhePheLeuLeu 460
31 TTGGCGCTGGCGCTTTCCCTCATCTCTCT 3

RESULT 9
US-11-266-748A-64946
; Sequence 64946, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64946
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (129)..(137)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-64946

Alignment Scores:
Pred. No.: 6.17e-95 Length: 1373
Score: 1350.00 Matches: 282
Percent Similarity: 67.3% Conservative: 35
Best Local Similarity: 59.9% Mismatches: 71
Query Match: 37.4% Indels: 85
DB: 8 Gaps: 7

US-10-719-202-2 (1-674) x US-11-266-748A-64946 (1-1373)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 181 ATGCTGTGGCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 240
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 241 CTGGAGAGCGCTTGTGGGCGCTCAGACGCTACCCACCTCTCTCTCTCTCTCTCTCTCT 300
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60

301 CTCTGGGACAGTGACATCTCTCCCTGCTGGGGACATCGTGCCTCGGCGCCCGGTG 360
61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
361 CTGGCGCTTACGCACCTGTCAGACAGAGCTGTGTCTGAGGTGCAGAGAGACCGACTGT 420
81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
421 GACCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459
101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 120
460 -----GCTCTCTCTCCAGGCCCA 477
121 ValValLeuSerPheGlnAlaLysProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
478 GTCTGTCTCTCTCTCCAGGCCCTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
538 CCTGCTGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 597
161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu 180
598 GCTGCCCTTAGGAGTGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
181 LeuAsnLeuThrGlnGlnLeuProAsp-----GlyAsp 191
658 CTCACGACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
192 AsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPheLeuLeuTrpLeu 211
717 AACGTGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 773
212 ArgProValProAspAlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsn 231
774 -----TGG-----AATCAGACTGGACCGCAGATC 797
232 IleThrLeuAsnHisThrAspLeuVal-ProCysLeuCysIleGlnValTrpSerLeuGln 251
798 ATTACCTTGAACACACAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 857
251 uproAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAs 271
858 ACCTGACTCGGTAGGACGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917
271 nLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaPr 291
918 CCTCTGGCAAGC-CGCGGACTGCGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 976
291 o-CysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysG 311
977 GTTGTCTGCTGCCCGCAGAGCGGCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1036
311 lnProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG 331
1037 AGCCACTGTGCTCCACCGCTTTCTTGGGAGATGTCTACTCTGTGGC-----1080
331 lnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGluLysValGlnL 351
1081 -----GTGAACAGCTCGGAGAGCTGAGC 1105
351 euGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValG 371
1106 TGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1165
371 luMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrP 391
1166 AGACACAGGCGCCCGCAGGACACAGATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1225
391 roLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuLeuGlnAspP 411
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148 CACTACCCAGCAAGCCCTCCACG-----126
Qy 411 heArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAspMetGlySerLeuTrpAlaC 431
Db 125 -----CTATGG---GACGATGACTTGGGAGCCCTATGGCCCT 92
Qy 431 ysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuL 451
Db 91 GCCCATGGACAAATATCATCCAAAGCGCTGGGGCCCTCGTGGCTGGCTGGCTGGCTACTCT 32
Qy 451 euAlaAlaLeuPhePheLeuLeu 460
Db 31 TTGGCGCTGGCTTTCCCTCATCTCCTCT 3

RESULT 11
US-11-293-697-313
; Sequence 313, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 313
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-313

Alignment Scores:
Pred. No.: 3,7e-75 Length: 1864
Score: 1096.50 Matches: 254
Percent Similarity: 65.2% Conservative: 53
Best Local Similarity: 53.9% Mismatches: 108
Query Match: 30.4% Indels: 56
DB: 8 Gaps: 15

US-10-719-202-2 (1-674) x US-11-293-697-313 (1-1864)
Qy 230 GlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal-----247
Db 431 CAGACATTGTAATAAATCAT-----ATAGTATCTTAAATTTGCATACAAATACCATGG 484
Qy 248 -----TrpSerLeuGlu-ProAs 253
Db 485 GAAAGGGATAAGGTGGGACTGGGTTGCAATTTTATAGAGGGTGGTGCATGTGAGAAAGGA 544
Qy 253 pSer-----GluArgValGluPheCysProPheArgGluAspProGlyAl 268
Db 545 ATCTCTTTGAGAGCTTAGATGAGAGGGGAACCATGCTCGTAAGA-----590
Qy 268 ahisArgAsnLeuTrpHisIleAlaArg-----LeuArgValLeuSerProGlyValTr 286
Db 591 -CATAAAAACAGCTTTTAGGTGTCAGAGACGCTTTATACAGATGATCTCACAGGC---TG 646
Qy 286 pGlnLeuAspAlaProCys-CysLeuProGlyLysValThrLeuCysTrpGlnAlaPro- 305
Db 647 GGGCAGAGAAAGA---TGTTAGTATCTTAATCACCAGCCTTGAATCCACATCTGCCTC 703
Qy 306 -----AspGlnSerProCysGlnProLeuValPro-----ProValProG 319
Db 704 AGGTCAGATTGAGTGCAGATTCCCAACCCCAACAGGCCTTCTGTTCCTGCCCCATT---759
Qy 319 lnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsn- 338
Db 760 -----CTGGTCTTCTGCTTGGCTTTGCTTTTCTTAGTGGC---CCTAAC 805

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RESULT 12
 US-11-266-748A-218328/c
 ; Sequence 218328, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:


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Db 61 GTGTGGCCCTCTGGAACCTGACTCGCTGTAGGACGAACATCTGCCCTCTCAGGAGGAGCCCC 120
Qy 267 GlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrp 286
Db 121 CGCGCACACCAAGAACTCTGCAAGCCGCCGACTGCGACTGCTGACCTCGACCTCGACAGCTGG 180
Qy 287 GlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAsp 306
Db 181 CTGCTGGAGCGACCGCTGCTGCTGCCCGCAGAGCGGCACCTGTGCTGGCGGCTCCGGGT 240
Qy 307 GlnSerProCysGlnProLeuValProValProGlnLysAsnAlaThrValAsnGlu 326
Db 241 GGGGACCCCTCCAGCCACTGCTGCCACCGTCTTCTGGGAGACGTCACCTGTGGACAAAG 300
Qy 327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrp 346
Db 301 GTTCTCGAGTTCCCATTTGCTGAAGGCCACCTTAACCTCTGTGTTCAAGTGAACAGCTCG 360
Qy 347 GluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAsp 366
Db 361 GAGAAGCTGCGAGCTGCGAGAGTGTGTGGGTGACTCCCTCGGGGCTCTCAAAAGACGAT 420
Qy 367 MetLeuValGluMetLysThrClyLeuAsnAsnThrSerValCysAlaLeuGluPro 386
Db 421 GTGCTACTGTGGAGACACGAGGCCGCCAGGACAAACAGATCCCTCTGTGCTTGGAAACC 480
Qy 387 SerGlyCysTrpProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 406
Db 481 AGTGGCTGTACTTCACTACCCAGCAAGCCCTCCAGAGGCGAGCTCGCTTGGAGATAC 540
Qy 407 LeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGly 426
Db 541 TTACTACAAGACCTGCACTGAGCCAGTGTGTCAGCTATGG--GACGATGACTTGGGA 597
Qy 427 SerLeuTrpAlaCysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeu 446
Db 598 GCGCTATGGCGCTGCCCATGACAAATACATCCCAAGCGCTGGGCCCTCTGTGTGGCTG 657
Qy 447 AlaCysLeuLeuAlaAlaLeuPhePheLeuLeuLysLysAspArgArg 466
Db 658 GCCTGCCCTACTTTTGGCGCTCGCTTTCCTCATCTCTCTCTCAAAAGGATCACGCG 717
Qy 467 Lys 467
Db 718 AAA 720
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RESULT 14
US-11-266-748A-293048
; Sequence 293048, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293048
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-293048

Alignment Scores:
Pred. No.: 3,86e-60 Length: 1000
Score: 897.50 Matches: 186
Percent Similarity: 74.2% Conservatives: 27
Best Local Similarity: 64.8% Mismatches: 53
Query Match: 24.9% Indels: 21
DB: 8 Gaps: 5

US-10-719-202-2 (1-674) x US-11-266-748A-293048 (1-1000)
Qy 393 ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArg 412
Db 1 CCCAGCAAAAGCCTCCACGAGGCGAGCTGCCCTTGGAGAGTACTTACTACAAGACCTGCGAG 60
Qy 413 SerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysPro 432
Db 61 TCAGGCCAGTGTCTGACGCTATGG--GACGATGACTTGGAGCGCTATGGGCTGCCCC 117
Qy 433 MetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAla 452
Db 118 ATGACAAATACATCCACAGCGCTGGGCCCTCGTGTGGCTGGCTGCTACTCTTTGGC 177
Qy 453 AlaAlaLeuPhePheLeuLeuLysLysAspArgArgLys----- 467
Db 178 GCTGGCTTTCCCTCATCTCTCTCAAAAGGATACACGCAAGAGGCTGGCTGAGGCTC 237
Qy 468 -----AlaAlaArgGlySerArgTrpAlaLeuLeuLeu 478
Db 238 TTGAACAGGAGCTCGCTCGGGGGCGCGCCAGCGGCG--CGCGCGCTCTGCTCTC 294
Qy 479 HisSerAlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeuSer 498
Db 295 TACTCAGCGATGACTCGGCTTTTCAGGCGCTGTGGGCGCCCTGCGCTGCGGCTGTCG 354
Qy 499 GlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGly 518
Db 355 CAGCTGCCGCTGCGCGTGGCGGTAGACCTGTGGAGCCCTGCTGTAACCTGAGCGCGCAGGG 414
Qy 519 AlaLeuAlaTrpPheHisGlnArgArgGlyLeuGlnGluGlyValValLeu 538
Db 415 CCCGTGGCTTGGTTTTCAGCGCGCGCGCCAGACCCCTGCAGAGAGGCGCGCTGGTGGTC 474
Qy 539 LeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnTrpVal 558
Db 475 TTGCTCTTCTCTCCCGTGGCGTGGCTGTGTGACGCGAGTGGCTCAGAGATGGGCTGTC 534
Qy 559 GluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuPro 575
Db 535 GGGCGCGGGCGCGACCGCGCCGACGCGCTTCCCGGCGCTCGCTCAGCTGCGTGGTGGCC 594
Qy 576 AspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTrpPheAspGlyLeuLeu 595
Db 595 GACTTCTTTCAGCGCGCGCGCGCGCGCTACGTGGGGCGCTGCTTTCACAGAGCTGCTC 654
Qy 596 HisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGln 615
Db 655 CACCCGAGCGCGCTTACCGCCCTTTTCGCGCACCGTGGCGCTCTCTACATCGCCCTCCCAA 714
Qy 616 LeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAla 635
Db 715 CTGCCAGACTTCTTGGGGGCCCTTGACGAGCGCTCGCGCCCGCGCTTCCGCGGCGCTCCAA 774
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REFERENCE	Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBLISHED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBLISHED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBLISHED	
REFERENCE	5
AUTHORS	The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBLISHED	
REFERENCE	6
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.
TITLE	Antisense transcription in the Mammalian Transcriptome
JOURNAL	Science 309, 1564-1566 (2005)
PUBLISHED	
REFERENCE	7
AUTHORS	The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE	The Transcriptional Landscape of the Mammalian Genome
JOURNAL	Science 309, 1559-1563 (2005)
PUBLISHED	8 (bases 1 to 973)
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

FEATURES	source	URL: http://genome.gsc.riken.jp/fantom.gsc.riken.jp/
	Location/Qualifiers	URL: http://genome.gsc.riken.jp/fantom.gsc.riken.jp/
	1..973	
	/organism="Mus musculus"	
	/mol_type="mRNA"	
	/strain="C57BL/6J"	
	/db_xref="FANTOM DB:A530050M19"	
	/db_xref="taxon:10090"	
	/clone="A530050M19"	
	/sex="male"	
	/tissue_type="aorta and vein"	
	/clone_lib="RIKEN full-length enriched mouse cDNA library"	
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	1..973	
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	Best Local Similarity:	85.3%
	Query Match:	33.4%
	Indels:	40
	Gaps:	1
	DB:	6
	US-10-719-202-2 (1-674) x AK040950 (1-973)	
QY	437	IleHisArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
DB	880	ATCCACAGGCGCTGGTCTCTAGTATGCTGGCTGCTACTCTTGGCTGGCGCTTTTC 821
QY	457	PhePheLeuLeuLeuLysAspArgArg-Lys----- 467
DB	820	TTCTTCTCTCTCTATAAAGGACCGCAGGAAAGTGAGTGTTCCTGCTGCTGTTTC 761
QY	467	----- 467
DB	760	CAAGGACAGTCTCAACAGTGGCGCTGGGGCTCAATTGGTGGAGGAGGAGGTCGG 701
QY	468	-----AlaAlaArgGlySerArgThrAlaLeu 477
DB	700	GCTCACCTCACAGGCTCCACTATCTCTGTAGCGCGCGTGGCTCCGCGCAGCGCTTGT 641
QY	477	uLeuHisSerAlaAspGlyAlaGlyTyTGluArgLeuValGlyAlaLeuAlaSerAlaLe 497
DB	640	CCTCCACTCGCGCAGCGAGCGGCTTACGAGCGTCTGGTGGAGCAGCTGGCGCTCGCGTT 581
QY	497	uSerGlnMetProLeuArgValAlaValaValaLeuTrpSerArgGluLeuSerAlaHi 517
DB	580	GAGCCAGATGCCACTCGGTGGCGCTGGACCTGTGAGCCCGCGCGGCTGAGCGCGCA 521
QY	517	sGlyAlaLeuAlaTrpPheHisGlnArgArgGileLeuGlnGluGlyGlyValVa 537
DB	520	CGGAGCCCTAGCTGTGTTCCACCACCGACGCGCGTATCTCTCAGAGGGGTGGTGGT 461
QY	537	lIleLeuLeuPheSerProAlaAlaValaGlnCysGlnGlnTrpLeuGlnGlnTh 557
DB	460	AATCTTCTCTTCTCGCGCGCGCTGGCGCAGTGTTCAGCAGTGGCTGCAGCTCCAGAC 401
QY	557	rValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPh 577
DB	400	AGTGGAGCGCGCGCGCGCTACGTCGGGGTCTACTTCAGCGGGCTGTGTCACCCGATTT 341
QY	577	eLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyPheAspGlyLeuLeuHisPr 597
DB	340	CCTGCAAGCGCGCGCGCGCTACGTCGGGGTCTACTTCAGCGGGCTGTGTCACCC 281
QY	597	oAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuPr 617
DB	280	AGACTCTGTGCGCGCTTCGCGCTTCGCGCTCTTCTCCCTGCGCTCGCAGCTGCC 221

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617 oAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspAr 637
220 GGCCTTCTCGATGACATGCGAGGAGGCTGCTCCACTTCCGGGGGCGACCCGGGACCG 161
637 qValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGl 657
160 GGTGGACAGTGTGACCCAGGCGCTGCGGTCCGCCCTGGACAGCTGTACTTCTAGCTCGGA 101
657 uAlaProGlyCysGluGlnTrpAspLeuGlyProCysThrThrLeuGlu 674
100 AGCCCCAGGCTGCTCGAGGAATGGACCTGGACCTGGACCTGCACTACACTAGAA 49

RESULT 8
LOCUS BG968034 784 bp mRNA linear EST 12-JUN-2001
DEFINITION 602832412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987035 5',
ACCESSION BG968034
VERSION BG968034.1 GI:14355671
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC http://mgs.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10997 row: g column: 04
High quality sequence stop: 646.
FEATURES
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1..784
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4987035"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 6.76e-96 Length: 784
Score: 1187.00 Matches: 233
Percent Similarity: 89.7% Conservative: 3
Best Local Similarity: 88.6% Mismatches: 18
Query Match: 32.9% Indels: 10
DB: 2 Gaps: 2
US-10-719-202-2 (1-674) x BG968034 (1-784)
234 LeuAenHisThrAspLeuValProCysLeuGlnGlyValTrpSerLeuGluProAsp 253
3 TTAACACACAGACCTGTTCCCTGCTCTGCAATTCAGGTGTGCTGAGACCCAGAC 62
254 SerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrp 273
63 TCTGAGAGGTGCAATTCTGCCCTTCCGGGAAGATCCCGGTGCACAGGAACCTCTGG 122

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274 HisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
123 CACATAGCCAGGCTGGGGTACTGTCCCGAGGGATATGGCAGCTAGATGGCCTTGCTGT 182
294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
183 CTCGCCGGCAGGTAACTACTGTCTGGCAGCCACAGACAGAGTCCCTGCCAGCCACTT 242
314 ValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuVal 333
243 GCGCCACCACTGTCGCCAGAGAAACGCACTGTGAATGAGCCACCAAGATTTCAGTTGGTG 302
334 AlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlnLysValGlnLeuAla 353
303 GCGAGGCCACCCCAACCTCTGTCTCCAGGTGAGCACCTGGGAGAGGTTACAGTGCACGCG 362
354 CysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLys 373
363 TGCTTGTGGGCTGACTCTCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAA 422
374 ThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuPro 393
423 ACCGCGCTCAACAACACATCAGTCTGTGCTTGAACCCAGTGGCTGTACACCATGCC 482
394 SerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSer 413
483 AGCATGAGCTCCACGAGAGCTGCTCGCTGGGAGAGGAGTTGCTGCACGACTTCCGATCA 542
414 HisGlnCys-MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMe 433
543 CACCAGTGTAAATGCAGCTGTGGACGATGACCAACATGGGATGCTATGGGCTGCCCAT 602
433 TAspLysTrpTyrIleHisArgArgTrpValLeuValTrpLeuAla-CysLeuLeuLeu-Ala 452
603 GGACAAAGTACATCCACAGGCGCTGGTACTAGTATGGTGGCTGACTACTCTCTGGGCT 662
453 -----AlaAlaLeuPhePheLeuLeuLysLysLysAspArgArg-LysAlaAlaAaR 470
663 GACGGCGCATTATCATCTACTCTCGCTCCATCTTAAGAAAAGGACCGAGGAAAGGGCCCG 722
470 gGlySerArg-----ThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGl 487
723 TGGGTCCCGGAACAGGGCAATTGCTTCC-CTCAGGCTCCGACGAGCGAGCGGGCTAAGA 781
487 u 487
782 A 782
RESULT 9
BG969618 1006 bp mRNA linear EST 26-OCT-2001
LOCUS BB609618 RIKEN full-length enriched, 18 days embryo Mus musculus
DEFINITION CDNA clone 1110025H02 5', mRNA sequence.
ACCESSION BB609618
VERSION BB609618.1 GI:16451334
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 1006)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

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SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 775)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through INL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:897119
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 495.
FEATURES
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1..775
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/notes="Organ: mammary gland; Vector: p773D-PacI; Site_1:
Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a
Not 1 - oligo(dT) primer [5'
TGTTACCATCTGCACTGAGCGCGCGCGAATGGTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-87 Length: 775
Score: 1095.00 Matches: 228
Percent Similarity: 90.0% Conservative: 5
Best Local Similarity: 88.0% Mismatches: 25
Query Match: 30.4% Indels: 4
DB: 1 Gaps: 0
US-10-719-202-2 (1-674) x AI007139 (1-775)
Qy 373 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeu 392
Db 3 AANAACGGCCCTCAACACACATCATGCTGTGCTTGGAAACCCAGTGGCTGTACACCACTG 62
Qy 393 ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArg 412
Db 63 CCCAGATGGCTCCACAGAGAGCTGCTCGCTGGAGAGAGTGTGCTGCAGAGATTCCGA 122
Qy 413 SerHisGlnCysMetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCysPro 432
Db 123 TCACACACAGTGTATCCAGCTGTGGACCATGACACATGGGATCGTATGGCGCTGCCCA 182
Qy 433 MetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAla 452

Db 183 TG-GACAGTACATCCACAGGCGCTGGGTCTCTAGTATGGCTGGCCTGCTACTCTTTGGCT 241
Qy 453 AlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySer 472
Db 242 GCGGCGCTTTCT 301
Qy 473 ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyLysLysArgLysValGlyAla 492
Db 302 CGCACCGCTTGTCT 361
Qy 493 LeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArg 512
Db 362 CTGGCGCTCCGCGTTGAGCCAGATGCCACTGCGCGCTGGCGCTGGACCTGTGGAGCCCGC 421
Qy 513 GluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisAlaArgArgGlyLeuGln 532
Db 422 GAGCTGAGCGCGACGAGCCCTAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 481
Qy 533 GluGlyGlyValValLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrp 552
Db 482 GAGGTGGCGTGTGTATCT 541
Qy 553 LeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCys 572
Db 542 CTGCAGCTCCACAGCAGTTGAGCGCGCGCGCATGACGCCCTCGCGCGCTTCTCTCTCTCTCT 601
Qy 573 ValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTrpPheAsp 592
Db 602 GTGCTTATCCGATTTTCTGCAAGC-CGGCGCGCGCTTAACCGTCGGGGTCTACTTCGAC 660
Qy 593 -GlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSerLe 612
Db 661 GGGCTGTCTGCAACCAAACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Qy 612 uProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer 630
Db 721 GCCTCGGCACCTTGC-ACCTTCTCTGGAATGACTTACGGAAGGTGATCAATTTCG 774
RESULT 11
BQ829429 597 bp mRNA linear EST 15-SEP-2002
LOCUS LL6in23107 APT024-subtracted library Mus musculus cDNA 5', mRNA
DEFINITION sequence.
ACCESSION BQ829429
VERSION BQ829429.1 GI:22861484
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS Hackney, J.A., Charbord, P., Brunk, B.P., Stoeckert, C.J.,
Lemischka, I.R. and Moore, K.A.
TITLE A molecular profile of a hematopoietic stem cell niche
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
PUBMED 12226475
COMMENT Contact: Moore, Kateri A.
Department of Molecular Biology
Princeton University
217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544,
USA
Tel: 609 258 0605
Fax: 609 258 2759
Email: kmoore@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for
gene products expressed by a hematopoietic stem cell-supporting
stromal cell line, APT024.
Seq primer: M13Reverse or T7.
Location/Qualifiers
1..597
/organism="Mus musculus"
/mol_type="mRNA"

the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH MGC 235) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

389 CAGTGTCCAGCAGTGGCTGACAGCTCCAGACAGTGGAGCCCGGCGCATGACGCCCTCGCC 330
 568 AlATrPLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrVal 587
 329 GCCTGGCTCAGCTGGCTACCGATTTCTGCAAGCCGGCGACCGGCCGCTACGTC 270
 588 GlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAla 607
 269 GGGGTCTACTTTCAGCGGGCTGCTGCACCCAGACTCTGTGCTCCCTCCCGTCCGGCTGCC 210
 608 ProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCys 627
 209 CGCTCTCTCTCCCTGCTCGCAGCTGCGGCTTTCTGATGCTGCTGAGGAGGCTGC 150
 628 SerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSer 647
 149 TCCACTTCGGGGGCGACCGCGACCGGGTGGAGTGACCCAGCGCTCGGCTCC 90
 648 AlaLeuAspSerCysThrSerSerSerGluAlaProGlyCysCysGluGluTTPAspLeu 667
 89 GCCCTGGAGAGCTGTACTTCTAGCTCGGAGCCCGAGGCTGCTGCGAGGAATGGACCTG 30
 668 GlyProCysThrThrLeuGlu 674
 29 GCGAGCTGCACACTAGAA 9

CK474183 739 bp mRNA linear EST 14-JAN-2004
 AGENCOURT 17619644 NIH_MGC 236 Rattus norvegicus cDNA clone
 IMAGE:7129543 5', mRNA sequence.

CK474183 1 GI:40818281
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 739)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@remail.nih.gov
 Tissue Procurement: Howard Jacobs
 cDNA Library Preparation: Express Genomics
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM15027 row: f column: 05
 High quality sequence stop: 661.
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 /clone="IMAGE:7129543"
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 /clone_lib="NIH MGC 236"
 /note="Organ: kidney; Vector: pExpress-1; Site: 1: EcoRV;
 Site 2: NotI; RNA obtained from pooled kidney tissue from
 a mix of male and female animals at 8 wk old. Tissues were
 snap-frozen and kept at -80C for two days before RNA
 extraction and purification (Tri-reagent method). cDNA was
 primed using oligo-dT primer.
 5'-pgactagttctatgacgagcgccgccc(7)25-3' and cloned into

ORIGIN

Alignment Scores: 1.99e-83 Length: 739
 Pred. No.: 1048.00 Matches: 190
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 Percent Similarity: 85.2% Mismatches: 36
 Best Local Similarity: 78.2% Indels: 0
 Query Match: 29.1% Gaps: 0
 DB:

US-10-719-202-2 (1-674) x CK474183 (1-739)

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 1 AATGTTCTTCTGATCTGGACGCTCTTAAGGAGCGAAATTTGGCTTCTTACTTACTCG 60
 212 ArgProValProAspAlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsn 231
 61 GATCAGGCCCGAGGCTCTCTCAATCTCTTGTGTACAAAACCTGACTGACCTCAGAAC 120
 232 IleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTTPSerLeuGlu 251
 121 ATTACTTTAAACCACTGACCTGTTCTCCCTGCTGCTGCTTATGTTATGTTCTAGGAG 180
 252 ProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 271
 181 CAGACTCTGTAGGACCCAGCTTCTGCCCCCTTCAAGAAAGATCCCGTGCACACAGAAC 240
 272 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTTPGlnLeuAspAlaPro 291
 241 CTTTGGCACAATGGCCAGGCTGGGGTGCAGTCTCTCAGGAGCTGGTCTAGACACGCT 300
 292 CysCysLeuProGlyLysValThrLeuLeuCysTTPGlnAlaProAspGlnSerProCysGln 311
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 481 CAAGAGTGTCTGGGCTGACTCTCTTAGGCCCTTCAAGGATGATATGCTGTAGTGAG 540
 372 MetLysThrGlyLysAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrPro 391
 541 ATGAAACCTGACCTAAACGACACATCAGTCTGTGCTTGGACCCAGTGGCTGTACCCA 600
 392 LeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGlnLeuGlnAspPhe 411
 601 CTGCTAGTGTGCTCCACGAGAGCTGCTGCCCTTGGAGAGCAGTGTGCTTCTAGACTTC 660
 412 ArgSerHisGlnCysMetGlnLeuTTPAsnAspAspAsnMetGlySerLeuTTPAlaCys 431
 661 AGGACACACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 432 ProMetAsp 434
 721 TCCATGGAC 729

RESULT 14
 CK770217/c 884 bp mRNA linear EST 20-FEB-2004
 LOCUS CK770217
 DEFINITION 958358 MARC 1BOV Bos taurus CDNA 3', mRNA sequence.

FEATURES
 source

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ACCESSION CK770217
VERSION CK770217.1 GI:42724311
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
        Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
        Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
        Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
        Quackenbush, J. and Keefe, J.W.
        1 (bases 1 to 884)
        Title: Sequence evaluation of four pooled-tissue normalized bovine cDNA
        libraries and construction of a gene index for cattle
        Genome Res. 11 (4), 626-630 (2001)

JOURNAL
PUBMED 11282978
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called with phred v0.020425.c and
        trimmed with the aid of the trim_alt option. Vector identified with
        cross_match v0.990329.
        Plate: 87 row: K column: 20
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                Library made from pooled tissue from lymph node, ovary,
                fat, hypothalamus, and pituitary."

FEATURES
source
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        /clone_lib="MARC 1BOV"
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        Library made from pooled tissue from lymph node, ovary,
        fat, hypothalamus, and pituitary."

ORIGIN
Alignment Scores:
Pred. No.: 1..25e-82 Length: 884
Score: 1040.50 Matches: 191
Percent Similarity: 78.5% Conservat: 28
Best Local Similarity: 68.5% Mismatches: 59
Query Match: 28.9% Indels: 1
DB: 5 Gaps: 1

US-10-719-202-2 (1-674) x CK770217 (1-884)
Qy 189 AspGlyAspValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeu 208
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Db 871 GATGGCGAGGACGTCGCGCTGTACTGAGCTCTCTGAGGAGCAGCGCTTCGGCCTCTCT 812
Qy 209 LeuTyrluLeuArgProValProAspAlaLeuLysSerLeuTrpTyrluAsnLeuThrGly 228
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 811 CTGTACTGGAAACACAGGTCACGGGCCCTATAAACCCCTGGTGGCACAGTAACTGACTGGA 752
Qy 229 ProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrp 248
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Qy 249 SerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAla 268
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Db 691 CCCCTGGAGCCGACTCTGTACAGACCCAGCATCTGCCCTTTAGGAGGAGACCCCGCGCA 632
Qy 269 HisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeu 288
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 631 CACCGAAACCTCTGGCGCGCTGCCCGGATTCAGCTGCTCCCGCTGGGAATGGCGGCTA 572
Qy 289 AspAlaProCysCysLeuProGlyLyLeValThrLeuCysTrpGlnAlaProAspGlnSer 308
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Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
 10 (11), 1757-1771 (2000)
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 Sugahara, Y. and Hayashizaki, Y.
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 non-redundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
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 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

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1. 643
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6J"
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  /clone="9330110N14"
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  /tissue_type="diencephalon"
  /dev_stage="adult"
  /lab_host="DH10B"
  /clone_libs="RIKEN full-length
  diencephalon"
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/lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, adult male
 diencephalon"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN, Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCGACGACCTCTTTTCTTTTCTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 185.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTCGATTAATTAATATCCCCCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified phluescript KS(+) after bulk excision
 from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
 BamHI"

ORIGIN

Alignment Scores:	1.03e-82	643
Pred. No.:	1039.00	197
Score:	99.5%	Matches: 1
Percent Similarity:	99.0%	Conservative: 1
Best Local Similarity:	28.8%	Mismatches: 1
Query Match:	7	Indels: 0
na		Gaps: 0

10-710-202-2 (1-674) x BB625706 (1-643)

Qy	476	LeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgIeuValGlyAlaLeuLlaSer	495
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Qy	496	AlaLeuSerGlnMetProLeuArgVallAlaValAspLeuTrpSerArgGluLeuSer	515
Dd	583	GCGTTGAGCCAGNTGCACCTGCGCGTGACCTGTGGAGCCGCCGAGCTGAGC	524
Qy	516	AlaHisGlyAlaLeuAlaIrrPheHisIstGlnArgArgGileLeuGlnGluGlyGly	535
			464

536	ValValIleLeuLeuPheSerProAlaValAlaGlnCysGlnGlnTrpLeuGlnLeu	555
463	GGGTAATCCTTCTTCCTCGCCCGGGCCGTGGCGAGTGTGAGTGGCTGCAGTCC	404
556	GlnThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuPro	575
403	CAGACAGTGGAGCCCGGGCCGCGATGACGCCCTCGCCGCTGGCTTACGCTCGTGTCTACCC	344
576	AspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeu	595
343	GATTTCTTCGAGGCCGGGCCACCGCCGCTACGTGGGGTCTTACTTCGACGGGCTGTG	284
596	HisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGln	615
283	CACCACAGACTCTGTGCCCTCGCCCGTTCCGGGTGCGCCCGCTCTTCTCCCTGCCCTCGCAG	224
616	LeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAla	635
223	CTGCGGGCTTCTCCTGGATGCACTGAGGAGGCTGCTCCACTTCGCGGGGGCAGCCGGC	164
636	AspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer	655
163	GACCGGGTGAACGAGTGACCCAGGCGCTGGGGTCCGCCCTGGGACAGCTGTACTTCTAGC	104
656	SerGluAlaProGlyCysCysGlnGlnTrpAspLeuGlyProCysThrThrLeuGlu	674
103	TCGGAGACCCAGGCTGCTGCGAGGAAATGGGACCTTGGGACCTGCATCACTAGAA	47

Search completed: August 17, 2006, 13:15:31
Job time : 6905 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3605	100.0	674	3	US-09-899-471-2	Sequence 2, Appli
2	3605	100.0	674	4	US-10-719-202-2	Sequence 2, Appli
3	3583	99.4	698	3	US-09-898-471-5	Sequence 5, Appli
4	3583	99.4	698	4	US-10-719-202-5	Sequence 5, Appli
5	3572.5	99.1	698	6	US-11-150-533-26	Sequence 26, Appli
6	3569.5	99.0	689	6	US-11-150-533-30	Sequence 30, Appli
7	3565	98.9	698	3	US-09-863-818A-8	Sequence 8, Appli
8	3565	98.9	698	4	US-10-749-144-8	Sequence 8, Appli
9	3565	98.9	698	5	US-10-924-667-8	Sequence 8, Appli
10	3562	98.8	698	3	US-09-866-050A-509	Sequence 509, App
11	3539	98.2	698	4	US-10-416-442A-75	Sequence 75, Appli
12	2352.5	65.3	692	3	US-09-899-471-8	Sequence 8, Appli
13	2352.5	65.3	692	4	US-10-458-647-2	Sequence 2, Appli
14	2352.5	65.3	692	4	US-10-719-202-8	Sequence 8, Appli
15	2352.5	65.3	692	6	US-11-150-533-2	Sequence 2, Appli
16	2348.5	65.1	449	6	US-11-150-533-27	Sequence 27, Appli
17	2339	64.9	705	3	US-09-874-503-14	Sequence 14, Appli
18	2339	64.9	705	3	US-09-816-744-14	Sequence 14, Appli
19	2339	64.9	705	3	US-09-747-259-14	Sequence 14, Appli
20	2339	64.9	705	3	US-09-908-827-14	Sequence 14, Appli
21	2339	64.9	705	4	US-10-006-867-162	Sequence 162, App
22	2339	64.9	705	4	US-10-053-586-598	Sequence 598, App
23	2339	64.9	705	4	US-10-063-547-162	Sequence 162, App
24	2339	64.9	705	4	US-10-000-157-14	Sequence 14, Appli
25	2339	64.9	705	4	US-10-063-551-162	Sequence 162, App
26	2339	64.9	705	4	US-10-174-590-598	Sequence 598, App
27	2339	64.9	705	4	US-10-176-758-598	Sequence 598, App

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Qy 481 ADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSTAHGALAWFHHQRRRILOEGGVWILL 540
Db 481 ADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSTAHGALAWFHHQRRRILOEGGVWILL 540
Qy 541 FSPAQAQCCQWLQLOTVPEPGPHDALAAWLSCVLPDFLOGRATGRYVGVYFDGLLHPDSV 600
Db 541 FSPAQAQCCQWLQLOTVPEPGPHDALAAWLSCVLPDFLOGRATGRYVGVYFDGLLHPDSV 600
Qy 601 PPSFRVAPLFLSLPTQLPAFLDALQGCSTSGRPAADRVERVTOALRSALDSCSTSSSEAPG 660
Db 601 PPSFRVAPLFLSLPTQLPAFLDALQGCSTSGRPAADRVERVTOALRSALDSCSTSSSEAPG 660
Qy 661 CCEWDLGPCTTLE 674
Db 661 CCEWDLGPCTTLE 674
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RESULT 2

US-10-719-202-2

; Sequence 2, Application US/10719202

; Publication No. US20040121388A1

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Murine Cytokine Receptor

; FILE REFERENCE: 00-46

; CURRENT APPLICATION NUMBER: US/10/719,202

; CURRENT FILING DATE: 2003-11-21

; PRIOR APPLICATION NUMBER: US/09/899,471

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 674

; TYPE: PRT

; ORGANISM: mouse

US-10-719-202-2

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Query Match 100.0%; Score 3605; DB 4; Length 674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LVPTRLOTELVRCPQKTDTCALRVVVVHLAVHGHWAEPPEAGKSDSELOESRNASLQAO 120
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Qy 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180
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Qy 301 CWQAPQSPQPLVPVPQKGNATVNEPQDFQLVAGHPNLCVQVSTWEKVLQACSWADSL 360
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Db 481 ADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSTAHGALAWFHHQRRRILOEGGVWILL 540
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Db 541 FSPAQAQCCQWLQLOTVPEPGPHDALAAWLSCVLPDFLOGRATGRYVGVYFDGLLHPDSV 600
Qy 601 PPSFRVAPLFLSLPTQLPAFLDALQGCSTSGRPAADRVERVTOALRSALDSCSTSSSEAPG 660
Db 601 PPSFRVAPLFLSLPTQLPAFLDALQGCSTSGRPAADRVERVTOALRSALDSCSTSSSEAPG 660
Qy 661 CCEWDLGPCTTLE 674
Db 661 CCEWDLGPCTTLE 674

RESULT 3
US-09-899-471-5
; Sequence 5, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-09-899-471-5

Query Match 99.4%; Score 3583; DB 3; Length 698;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

Qy 1 MPVSWFLLSLALGRNPVVVLSLERLMEPQDTARCSLGLSCHLWDGVDVCLPGSLQAPGPV 60
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Qy 61 LVPTRLOTELVRCPQKTDTCALRVVVVHLAVHGHWAEPPEAGKSDSELOESRNASLQAO 120
Db 61 LVPTRLOTELVRCPQKTDTCALRVVVVHLAVHGHWAEPPEAGKSDSELOESRNASLQAO 120
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Db 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180
Qy 181 LNLTLQPLDGDNVLLTLDSVEEQDFSLLYLRPVPD 216
Db 181 LNLTLQPLDGDNVLLTLDSVEEQDFSLLYLRPVPD 240
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Db 241 ALKSLWYKNTLTPQNTLNTDLYVPCICIQWSLEPDSERVFECPPFPDGAHNLWHIA 300
Qy 277 RLRVLSPGVWQDAPCCLPCKVTILCQWAPQSPQPLVPVPQKGNATVNEPQDFQLVAGH 336
Db 301 RLRVLSPGVWQDAPCCLPCKVTILCQWAPQSPQPLVPVPQKGNATVNEPQDFQLVAGH 360
Qy 337 PNLVCQVSTWEKVLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGCTPLPSMA 396
Db 361 PNLVCQVSTWEKVLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGCTPLPSMA 420
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Db 481 FFLLLKKDRKKAARGSRRTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
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Qy 577 FLOGRATGRVGVYFDGLLHPDSVPSPRVAPLPSLPTQLPAFLDALOGGCGSTSAGRPA 636
Db 601 FLOGRATGRVGVYFDGLLHPDSVPSPRVAPLPSLPTQLPAFLDALOGGCGSTSAGRPA 660
Qy 637 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 674
Db 661 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 698

RESULT 4
US-10-719-202-5
; Sequence 5, Application US/10719202
; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-10-719-202-5

Query Match 99.4%; Score 3583; DB 4; Length 698;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;
Qy 1 MPVSWFLLSLALGRNPVWSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Db 1 MPVSWFLLSLALGRNPVWSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Qy 61 LVPTRLQTELVLRCPOKTDICALRVVVVHLAVHGHWAEPBEAGKSDSELQESRNASLQAQ 120
Db 61 LVPTRLQTELVLRCPOKTDICALRVVVVHLAVHGHWAEPBEAGKSDSELQESRNASLQAQ 120
Qy 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Qy 181 LNIITQQLP-----DGDNVLLTLDVSEEDFSLYLVRPVD 216
Db 181 LNIITQQLPDCRGLEVRDSIQSCVLPWLNSTGDGNDVLLTLDVSEEDFSLYLVRPVD 240
Qy 217 ALKSLWYKNTLGPQNTLNHTDLVPCICIQWSLEPDSERVEFCPPREDPGAHRNLWHIA 276
Db 241 ALKSLWYKNTLGPQNTLNHTDLVPCICIQWSLEPDSERVEFCPPREDPGAHRNLWHIA 300
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Db 301 RLRVLSFGVWQOLDAPCCLPKGVTLQWQADPQSPQPLVPPVQKNATVNEPQDFQVAGH 360
Qy 337 PNLVCQVSTWEKVOQACSWADSLGPPKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMA 396
Db 361 PNLVCQVSTWEKVOQACSWADSLGPPKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMA 420
Qy 397 STRAARLGEELLQDFRSHQCQMLWDDNMGSLMACPMDKYIHRRWLVWLACLLAAALF 456

Db 421 STRAARLGEELLQDFRSHQCQMLWDDNMGSLMACPMDKYIHRRWLVWLACLLAAALF 480
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Db 481 FFLLLKKDRKKAARGSRRTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
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Db 541 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQWLQLOTVFPGPHDALAAMLSCVLPD 600
Qy 577 FLOGRATGRVGVYFDGLLHPDSVPSPRVAPLPSLPTQLPAFLDALOGGCGSTSAGRPA 636
Db 601 FLOGRATGRVGVYFDGLLHPDSVPSPRVAPLPSLPTQLPAFLDALOGGCGSTSAGRPA 660
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Db 661 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 698

RESULT 5
US-11-150-533-26
; Sequence 26, Application US/111150533
; Publication No. US2006002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-150-533-26

Query Match 99.1%; Score 3572.5; DB 6; Length 683;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 671; Conservative 1; Mismatches 2; Indels 9; Gaps 1;
Qy 1 MPVSWFLLSLALGRNPVWSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Db 1 MPVSWFLLSLALGRNPVWSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Qy 61 LVPTRLQTELVLRCPOKTDICALRVVVVHLAVHGHWAEPBEAGKSDSELQESRNASLQAQ 120
Db 61 LVPTRLQTELVLRCPOKTDICALRVVVVHLAVHGHWAEPBEAGKSDSELQESRNASLQAQ 120
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Db 181 LNIITQQLPVLVPLNVSTGDGNDVLLTLDVSEEDFSLYLVRPVDALKSLWYKNTLGPQNT 240
Qy 232 ITLNHTDLVPCICIQWSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSPGVWQOLDAP 291
Db 241 ITLNHTDLVPCICIQWSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSPGVWQOLDAP 300
Qy 292 CCLPGKVTLCWQADPQSPQPLVPPVQKNATVNEPQDFQVAGHNLVCQVSTWEKVOQ 351
Db 301 CCLPGKVTLCWQADPQSPQPLVPPVQKNATVNEPQDFQVAGHNLVCQVSTWEKVOQ 360

352 QACSWADSLGPKDDMLLVEMKTLNNTSVCALEPSCGCTPLPMSASTRAARLGEELIQDF 411
361 QACUWADSLGPKDDMLLVEMKTLNNTSVCALEPSCGCTPLPMSASTRAARLGEELIQDF 420
412 RSHQCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLAALLAAALFFFLKLLKDRKAARG 471
421 RSHQCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLAALLAAALFFFLKLLKDRKAARG 480
472 SRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHRRIL 531
481 SRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHRRIL 540
532 QEGGVWILLFSPAFAVACQWMLQOTVEPFGPHDALAAWLSVLPDFLQGRATGRVGVYF 591
541 QEGGVWILLFSPAFAVACQWMLQOTVEPFGPHDALAAWLSVLPDFLQGRATGRVGVYF 600
592 DGLLHPDSVPSPFRVAPLFSPTQLPAFLDALQGGCSTSAGRPADRVERVTQALRSALDS 651
601 DGLLHPDSVPSPFRVAPLFSPTQLPAFLDALQGGCSTSAGRPADRVERVTQALRSALDS 660
652 CTSSEAPGCCCEWDLGPCTTLE 674
661 CTSSEAPGCCCEWDLGPCTTLE 683

RESULT 6
US-11-150-533-30
; Sequence 30, Application US/111150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-150-533-30

Query Match 99.0%; Score 3569.5; DB 6; Length 689;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 671; Conservative 1; Mismatches 2; Indels 15; Gaps 1;
QY 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGVDVLCPLGSLQASAPGV 60
DB 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGVDVLCPLGSLQASAPGV 60
QY 61 LVPTRLQTELVLRCPOKTDCAALRVVHVLAHGHWAEPPEAGKSDSELSQESRNASLOAQ 120
DB 61 LVPTRLQTELVLRCPOKTDCAALRVVHVLAHGHWAEPPEAGKSDSELSQESRNASLOAQ 120
QY 121 VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGARVQIWSYTKPRYQKE 180
DB 121 VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGARVQIWSYTKPRYQKE 180
QY 181 LNTQOLP-----DGDVLLTLDVSEBQDFSLYLRLPVPDALKSLWYKN 225
DB 181 LNTQOLPDCRGLEVRDSIQSCWDGDNVLLTLDVSEBQDFSLYLRLPVPDALKSLWYKN 240
QY 226 LTGPQNTTLNHTDLVPLCLIQVWSLEPDSERVEPCFPREDPGAHRNLWHIARLVLSPGV 285

241 LTGPQNTTLNHTDLVPLCLIQVWSLEPDSERVEPCFPREDPGAHRNLWHIARLVLSPGV 300
286 WQLDAPCCLLPGKVTLCWQAPDQSPCOPLPVPPQKNAVTNEPQDFQIVAGHPNLCVQVST 345
301 WQLDAPCCLLPGKVTLCWQAPDQSPCOPLPVPPQKNAVTNEPQDFQIVAGHPNLCVQVST 360
346 WEKVQLOACSWADSLGPKDDMLLVEMKTLNNTSVCALEPSCGCTPLPMSASTRAARLGE 405
361 WEKVQLOACSWADSLGPKDDMLLVEMKTLNNTSVCALEPSCGCTPLPMSASTRAARLGE 420
406 ELQDQFRSHQCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLAALLAAALFFFLKLLKDR 465
421 ELQDQFRSHQCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLAALLAAALFFFLKLLKDR 480
466 RKAARSGRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFH 525
481 RKAARSGRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFH 540
526 ORRRILOEGGVWILLFSPAFAVACQWMLQOTVEPFGPHDALAAWLSVLPDFLQGRATGR 585
541 ORRRILOEGGVWILLFSPAFAVACQWMLQOTVEPFGPHDALAAWLSVLPDFLQGRATGR 600
586 YGVYFDGLLHPDSVPSPFRVAPLFSPTQLPAFLDALQGGCSTSAGRPADRVERVTQAL 645
601 YGVYFDGLLHPDSVPSPFRVAPLFSPTQLPAFLDALQGGCSTSAGRPADRVERVTQAL 660
646 RSALDCTSSEAPGCCCEWDLGPCTTLE 674
661 RSALDCTSSEAPGCCCEWDLGPCTTLE 689

RESULT 7
US-09-863-818A-8
; Sequence 8, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-863-818A-8

Query Match 98.9%; Score 3565; DB 3; Length 698;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 671; Conservative 1; Mismatches 2; Indels 24; Gaps 1;
QY 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGVDVLCPLGSLQASAPGV 60
DB 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGVDVLCPLGSLQASAPGV 60
QY 61 LVPTRLQTELVLRCPOKTDCAALRVVHVLAHGHWAEPPEAGKSDSELSQESRNASLOAQ 120
DB 61 LVPTRLQTELVLRCPOKTDCAALRVVHVLAHGHWAEPPEAGKSDSELSQESRNASLOAQ 120
QY 121 VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGARVQIWSYTKPRYQKE 180
DB 121 VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGARVQIWSYTKPRYQKE 180
QY 181 LNTQOLP-----DGDVLLTLDVSEBQDFSLYLRLPVPD 216
DB 181 LNTQOLPDCRGLEVRDSIQSCWVLPWLVNSTDGDNVLLTLDVSEBQDFSLYLRLPVPD 240
QY 217 ALKSLWYKNLTGPQNTTLNHTDLVPLCLIQVWSLEPDSERVEPCFPREDPGAHRNLWHIARLVLS 276

[illegible]

Query Match	Best Local Similarity	98.9%;	Score 3565;	DB 4;	Length 698;
Matches 671;	Conservative 1;	Mismatches 2;	Indels 24;	Gaps 1;	
Qy 1	MPVSWFLLSALGRNPVVVSLRLMEPQDTARCSLGLSCHLWDGDLVCLPGSLQSA	PGPV 60			
Db 1	MPVSWFLLSALGRNPVVVSLRLMEPQDTARCSLGLSCHLWDGDLVCLPGSLQSA	PGPV 60			
Qy 61	LVPTRLQTELVLRCPOKTDICALRVVVHLAVHGHWAPEEAGKSDSELOSRNAS	LQQA 120			
Db 61	LVPTRLQTELVLRCPOKTDICALRVVVHLAVHGHWAPEEAGKSDSELOSRNAS	LQQA 120			
Qy 121	VVLSFQAYPIARCALLEVQVPADLVQPGQSVGSVDFCFEASLGAEVQIWSYTKPRYQKE	180			
Db 121	VVLSFQAYPIARCALLEVQVPADLVQPGQSVGSVDFCFEASLGAEVQIWSYTKPRYQKE	180			
Qy 181	LNLTQOLP-----DGNVLLTLDVSEEQDPSFLLYLRPVPD	216			
Db 181	LNLTQOLPDCRGLEVRDSTQSCWVLPWLVNSTDGNVLLTLDVSEEQDPSFLLYLRPVPD	240			
Qy 217	ALKSLYKGLTQPNITLNHTDLVPLCLCIQWMSLEPDSERVEFCPPFPREDPGAHNLWHIA	276			


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QY 217 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGAHNLWHIA 276
Db 241 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGAHNLWHIA 300
QY 277 RLRVLSFGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNAVNEPQDFQLVAGH 336
Db 301 RLRVLSFGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNAVNEPQDFQLVAGH 360
QY 337 PNLGVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 396
Db 361 PNLGVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 420
QY 397 STRAARLGEELLQDFRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 456
Db 421 STRAARLGEELLQDFRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 480
QY 457 FFLLLKKDORRKAARGSTRALLHSHADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLLLKKDORRKAARGSTRALLHSHADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
QY 517 HGALAWFHQRRIILOEGGVVILLFSPAQAQCOQWLQLOTVPGPHDALAAWLSCVLPD 576
Db 541 HGALAWFHQRRIILOEGGVVILLFSPAQAQCOQWLQLOTVPGPHDALAAWLSCVLPD 600
QY 577 FLOGRATGRYGVYFDGLLHPDVSPPRVAFLFSLPTQLPAFLDALQGGCSTSGRPA 636
Db 601 FLOGRATGRYGVYFDGLLHPDVSPPRVAFLFSLPTQLPAFLDALQGGCSTSGRPA 660
QY 637 RVERVTQALRSALDSCSTSSSEAPGCCCEWDLGPCTTLE 674
Db 661 RVERVTQALRSALDSCSTSSSEAPGCCCEWDLGPCTTLE 698

RESULT 10
US-09-866-050A-509
; Sequence 509, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 509
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-509

Query Match 98.8%; Score 3562; DB 3; Length 698;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 670; Conservative 2; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDTARCSGLSHLMDGVDVLCPLGSLQSPGPV 60
Db 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDTARCSGLSHLMDGVDVLCPLGSLQSPGPV 60
QY 61 LVPTRQLTELVLRCPOKTCALVRVWVHLVGHWAEPPEACKSSELQESRNASLQAO 120
Db 61 LVPTRQLTELVLRCPOKTCALVRVWVHLVGHWAEPPEACKSSELQESRNASLQAO 120
QY 121 VVLSFOAYPIARCALLEVQVPADLVQPGSVGSAVDFCDCEASLGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFOAYPIARCALLEVQVPADLVQPGSVGSAVDFCDCEASLGAEVQIWSYTKPRYQKE 180
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QY 181 LNTLQQLP-----DGDNVLLTLDVSEEDQFSELLYLRPVDP 216
Db 181 LNTLQQLPDCRGLEVRDSIQSCWVLPWLNVTSDGDNVLLTLDVSEEDQFSELLYLRPVDP 240
QY 217 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGAHNLWHIA 276
Db 241 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGAHNLWHIA 300
QY 277 RLRVLSFGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNAVNEPQDFQLVAGH 336
Db 301 RLRVLSFGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNAVNEPQDFQLVAGH 360
QY 337 PNLGVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 396
Db 361 PNLGVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 420
QY 397 STRAARLGEELLQDFRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 456
Db 421 STRAARLGEELLQDFRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 480
QY 457 FFLLLKKDORRKAARGSTRALLHSHADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLLLKKDORRKAARGSTRALLHSHADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
QY 517 HGALAWFHQRRIILOEGGVVILLFSPAQAQCOQWLQLOTVPGPHDALAAWLSCVLPD 576
Db 541 HGALAWFHQRRIILOEGGVVILLFSPAQAQCOQWLQLOTVPGPHDALAAWLSCVLPD 600
QY 577 FLOGRATGRYGVYFDGLLHPDVSPPRVAFLFSLPTQLPAFLDALQGGCSTSGRPA 636
Db 601 FLOGRATGRYGVYFDGLLHPDVSPPRVAFLFSLPTQLPAFLDALQGGCSTSGRPA 660
QY 637 RVERVTQALRSALDSCSTSSSEAPGCCCEWDLGPCTTLE 674
Db 661 RVERVTQALRSALDSCSTSSSEAPGCCCEWDLGPCTTLE 698

RESULT 11
US-10-416-442A-75
; Sequence 75, Application US/10416442A
; Publication No. US20040171109A1
; GENERAL INFORMATION:
; APPLICANT: Haudenschild, Dominik
; APPLICANT: Rose, Larry
; APPLICANT: Moseley, Timothy
; APPLICANT: Reddi, A. Hari
; TITLE OF INVENTION: IL-17 Receptor-Like Protein, Uses Thereof, and
; TITLE OF INVENTION: Modulation of Catabolic Activity of IL-17 Cytokines on
; TITLE OF INVENTION: Bone and Cartilage
; FILE REFERENCE: 023070-115511US
; CURRENT APPLICATION NUMBER: US/10/416,442A
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/247,134
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/271,197
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/328,904
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: WO PCT/US01/43855
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse IL-17RL
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(698)
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OTHER INFORMATION: Xaa = any amino acid
US-10-416-442A-75

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Query Match      98.2%; Score 3539; DB 4; Length 698;
Best Local Similarity 95.4%; Pred. No. 9.3e-318;
Matches 666; Conservative 1; Mismatches 7; Indels 24; Gaps 1;

QY 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGDLCLPGSLQSAAGPV 60
DB 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGDLCLPGSLQSAAGPV 60

QY 61 LVPTRLOTELVLRCPOKTDALRVVVHVLAVHGHWAEPPEAGKSDSELOESRNASLOAQ 120
DB 61 LVPTRLOTELVLRCPOKTDALRVVVHVLAVHGHWAEPPEAGKSDSELOESRNASLOAQ 120

QY 121 VVLSFOAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPYOKE 180
DB 121 VVLSFOAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPYOKE 180

QY 181 LNTLTOQLP-----DGDNVLLTLDVSEEQDFSLLYLRPVPD 216
DB 181 LNTLTOQLPDCRGLEVRDSIQSCWVLPWLVNSTDGDNVLLTLDVSEEQDFSLLYLRPVPD 240

QY 217 ALKSLWYKNTLGTQNTLNTDVLPCICIQVWSLEPDSERVEPCFPREDPGAHRNLWHIA 276
DB 241 ALKSLWYKNTLGTQNTLNTDVLPCICIQVWSLEPDSERVEPCFPREDPGAHRNLWHIA 300

QY 277 RLRLVSPGVWQDAPCLPGKVTLCQWAPDQSPQPLVPPVPQKNATVNEPQDPLVAGH 336
DB 301 RLRLVSPGVWQDAPCLPGKVTLCQWAPDQSPQPLVPPVPQKNATVNEPQDPLVAGH 360

QY 337 PNLGVQVSTWEKVLQACSWADSLGPFKODMLLVEMKTLGNNTSVCALEPSGCTPLPSMA 396
DB 361 PNLGVQVSTWEKVLQACSWADSLGPFKODMLLVEMKTLGNNTSVCALEPSGCTPLPSMA 420

QY 397 STRAARLGSELLQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLVLACILLAAALF 456
DB 421 STRAARLGSELLQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLVLACILLAAALF 480

QY 457 FPLLLKKDRKKAARGSTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRRELSA 516
DB 481 FPLLLKKDRKKAARGSTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRRELSA 540

QY 517 HGALAWFHRRRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAALSCVLPD 576
DB 541 HGALAWFHRRRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAALSCVLPD 600

QY 577 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPAD 636
DB 601 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPAD 660

QY 637 RVERVTOALRSALDSCTSSSEAPGCCCEWDLGPTTILE 674
DB 661 RVERVTOALRSALDSCTSSSEAPGCCCEWDLGPTTILE 698

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RESULT 12
US-09-899-471-8
; Sequence 8, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Human
US-09-899-471-8

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Query Match      65.3%; Score 2352.5; DB 3; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGDLCLPGSLQSAAGPV 60
DB 1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSGLSCHLWDGDLCLPGSLQSAAGPV 60

QY 61 LVPTRLOTELVLRCPOKTDALRVVVHVLAVHGHWAEPPEAGKSDSELOESRNAS 116
DB 61 LVPTRLOTELVLRCPOKTDALRVVVHVLAVHGHWAEPPEAGKSDSELOESRNAS 120

QY 117 LQAQVVLSEFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPR 176
DB 121 LQAQVVLSEFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLLYLRPVPDALKWYKNTL 227
DB 181 YQKELNLTQQLPALPWLNVNSADGDNVHLVNLVSEEQHFGLSLYWNVQVQPPKPRWHKNTL 240

QY 228 GPONITLNTDVLPCICIQVWSLEPDSERVEPCFPREDPGAHRNLWHIARLRLVSPGVQ 287
DB 241 GPONITLNTDVLPCICIQVWSLEPDSERVEPCFPREDPGAHRNLWHIARLRLVSPGVQ 300

QY 288 LDAPCCLPGKVTLCQWAPDQSPQPLVPPVPQKNATVNEPQDPLVAGHNLVCVQVSTWE 347
DB 301 LDAPCCLPGKVTLCQWAPDQSPQPLVPPVPQKNATVNEPQDPLVAGHNLVCVQVSTWE 360

QY 348 KVQLQACSWADSLGPFKODMLLVEMKTLGNNTSVCALEPSGCTPLPSMASTRARLGEEL 407
DB 361 KLQLOQCLWADSLGPFKODMLLVEMKTLGNNTSVCALEPSGCTPLPSMASTRARLGEEL 420

QY 408 LQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLVLACILLAAALFFILLKKDRK 467
DB 421 LQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLVLACILLAAALFFILLKKDRK 479

QY 468 AARGSTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRRELISAHGALAWFHQR 527
DB 480 AARGSTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRRELISAHGALAWFHQR 539

QY 528 RRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAALSCVLPDPLQGRATG 584
DB 540 RRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAALSCVLPDPLQGRATG 599

QY 585 RYGVYVFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPADRVERVTOA 644
DB 600 SYVGACDFRLLHPDAVPALEFRTVVPVFTPLPSQLPAPFLDALQGGCSTSAGRPADRVERVTOA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 13
US-10-458-647-2
; Sequence 2, Application US/10458647
; Publication No. US20030199041A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Pownder, Sarah L.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-50
; CURRENT APPLICATION NUMBER: US/10/458,647
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/608,918
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 692
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-458-647-2
Query Match      65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLLSLALGRNPVVSLERLMEPQDTARCSLGLSCHLWDGVLCPGLSQSAPGPV 60
DB 1 MPVWFLLSLALGRSPVLSLERLVGPQDATHCFGLSCLRWSDILCLPGDIIVAPGPV 60

QY 61 LVPRLQTELVLRCQKTCDCALRVVVVHLAVHGHWAEPPE-----AGKSDSELOESRNAS 116
DB 61 LAPHLQTELVLRCQKTCDCALRVAVHLAVHGHWEPEDEEKFAGGADSGVEEPRNAS 120

QY 117 LOAQVVLFSQAYPIARCALLEVQPADLVQGSVGSVAVFCFEASLGAEVQIWSYTKPR 176
DB 121 LOAQVVLFSQAYPIARCALLEVQPAALVQGSVGSVVYDCFEALGSEVRINWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLLYLRPVPDALKSLWYKNLT 227
DB 181 YKELNHTQQLPALPWLNVNSADGDNVHLVNVSEEQHFGLSLYWNQVQ3PPKPRWHKNLT 240

QY 228 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRLNWHIARLVLSPGVWQ 287
DB 241 GPQIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLQSWL 300

QY 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAIVNEPQDFQLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPAEALCWRAAPGDCQCPPLVPLSWENVTVDKLEFLLKXHPNLCVQVNSSE 360

QY 348 KYVQLQACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSGCTPLPSMASTAAARLGBEL 407
DB 361 KLQLEQCLWADSLGPKLDVLLLETRGPQDNRSICALPSGCTSLPSKASTAAARLGBYL 420

QY 408 LDQFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 467
DB 421 LDQLQSGCQLQLW-DDDLGALWACPMCKYIHKRWALVWLACLLFAAALLSLLLKKDHAK 479

QY 468 AARGSTALLHSADGAGYERLVGALASALSQWPLRVAVDLWSRRELSAHGALAWFHQR 527
DB 480 AARGRAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFVHAQR 539

QY 528 RRLQEGGVVILLFSPAQAACQWMLQOTVEP---GPHDALAAWLSVLPDFLQGRATG 584
DB 540 RQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGAGHPHDAFRASLSVLPDFLQGRAPG 599

QY 585 RYVGVYFDGLLHDPDSVPSRPAVPLFSLPTQLPAFLDALQGGCSTSGAGRPADRVERTQA 644
DB 600 SYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRAPRSGLQERAEQVSRA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 14
US-10-719-202-8
; Sequence 8, Application US/10719202
; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 692
; TYPE: PRT

; ORGANISM: Human
US-10-719-202-8
Query Match      65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLLSLALGRNPVVSLERLMEPQDTARCSLGLSCHLWDGVLCPGLSQSAPGPV 60
DB 1 MPVWFLLSLALGRSPVLSLERLVGPQDATHCFGLSCLRWSDILCLPGDIIVAPGPV 60

QY 61 LVPRLQTELVLRCQKTCDCALRVVVVHLAVHGHWAEPPE-----AGKSDSELOESRNAS 116
DB 61 LAPHLQTELVLRCQKTCDCALRVAVHLAVHGHWEPEDEEKFAGGADSGVEEPRNAS 120

QY 117 LOAQVVLFSQAYPIARCALLEVQPADLVQGSVGSVAVFCFEASLGAEVQIWSYTKPR 176
DB 121 LOAQVVLFSQAYPIARCALLEVQPAALVQGSVGSVVYDCFEALGSEVRINWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLLYLRPVPDALKSLWYKNLT 227
DB 181 YKELNHTQQLPALPWLNVNSADGDNVHLVNVSEEQHFGLSLYWNQVQ3PPKPRWHKNLT 240

QY 228 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRLNWHIARLVLSPGVWQ 287
DB 241 GPQIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLQSWL 300

QY 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAIVNEPQDFQLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPAEALCWRAAPGDCQCPPLVPLSWENVTVDKLEFLLKXHPNLCVQVNSSE 360

QY 348 KYVQLQACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSGCTPLPSMASTAAARLGBEL 407
DB 361 KLQLEQCLWADSLGPKLDVLLLETRGPQDNRSICALPSGCTSLPSKASTAAARLGBYL 420

QY 408 LDQFRSHQCMQWLNDDNMGSLWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 467
DB 421 LDQLQSGCQLQLW-DDDLGALWACPMCKYIHKRWALVWLACLLFAAALLSLLLKKDHAK 479

QY 468 AARGSTALLHSADGAGYERLVGALASALSQWPLRVAVDLWSRRELSAHGALAWFHQR 527
DB 480 AARGRAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFVHAQR 539

QY 528 RRLQEGGVVILLFSPAQAACQWMLQOTVEP---GPHDALAAWLSVLPDFLQGRATG 584
DB 540 RQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGAGHPHDAFRASLSVLPDFLQGRAPG 599

QY 585 RYVGVYFDGLLHDPDSVPSRPAVPLFSLPTQLPAFLDALQGGCSTSGAGRPADRVERTQA 644
DB 600 SYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRAPRSGLQERAEQVSRA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 15
US-11-150-533-2
; Sequence 2, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
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; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-150-533-2

Query Match          65.3%; Score 2352.5; DB 6; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

Qy      1  MPVSWFLLSLALGRNPVWSLERLMEPDTRACSLGLSCHLWDGDLVLCPSLOSAGPGV 60
Db      1  MPVPWFLLSLALGRSPVLSLERLVGPQDATHCPSGLSCRLWDSIDLCPGDIVPAPGPV 60

Qy      61  LVPTRLQTELVLRCPOKTDCAIRVVRVVHLAVGHWAEPBEB---AGKSDSELOESRNAS 116
Db      61  LAPHLQTELVLRCQKTDCCDLRLVAVHLAVGHWEPEDEBEKFGGADSGVEPRNAS 120

Qy      117  LQAQVLSFOAYPIARCALLLEVQPADLVQPGQSGSAVDFPCFEASLGAEYQIWSYTKPR 176
Db      121  LQAQVLSFOAYPIARCVLLEVQPAALVQPGQSGSVVYDFCEAALGSEVRIWSYTKPR 180

Qy      177  YQKELNLTQQLP-----DGNVLLTLDVSEEDQPSFLLYLRVPVDALKSLWYKNLT 227
Db      181  YKELNHTQQLPALPWLNVSGADGNVHLVNVSEQHFGLSLYWNQVQGGPKPRWHKNLT 240

Qy      228  GPONITLNHTDLVPLCLCIQWLSLPPDSERVEFCFPREDPGAHRLNHLIARLVLSPGVQ 287
Db      241  GPQITITLNHTDLVPLCLCIQWLPEDSVRTNICFPREDPRAHQNLWQARLRLTLQSWL 300

Qy      288  LDAPCCLPGKVTLQWAPDQSPCQPLVPPVQKNAVNEPDQFOLVAGHPNLCVQVSTWE 347
Db      301  LDAPCSLPAAALCWAPGGDPCCQPLVPLSWENVTVDKVLEFPFLKGHPLNLCVQVNSSE 360

Qy      348  KVQLQACSWADSLGPPFDDMLLVEMKTLNNTSVCALEPSCCTPLPSMASTFAARLGEEL 407
Db      361  KLQLQECWLWADSLGPLKDDVLLLETRGPQDNRSICALEPSCCTSLPSKASTFAARLGEYL 420

Qy      408  LQDPRSHQCMLWMDNNMGSILWACPMDKYIHRRVVLVWLACLLIAAALFPFLLLKCDORRK 467
Db      421  LQDLQSGCQLWLW-DDDLGALWACPMDKYIHKRWALVWLACLLIPAAALSLTLLLKCDHAK 479

Qy      468  AARGSRFTALLSHSADGAGYERLVGALASALSQMPLRVAVDWLSRRLELSAHGALAWFHQR 527
Db      480  AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDWLSRRLELSAQGFVAWFRAQR 539

Qy      528  RRILQEGGVILLIPSPAQAQCQWILQLTVEP---GPHDALAWLSCVLPDFLQCRATG 584
Db      540  RQTLQEGGVVILLIPSPGAVALCSEWLQDGVSGPGAHPDHAFRASLSCVLPDFLQGRAPG 599

Qy      585  RYGVGVYDGLLHPDSVSPFRVAPLPSLPTQLPAFLDALQCGCSTSGRPAADRVERVTOA 644
Db      600  SYVGACEDRLHPDAVPALEFRTVPVFTLPSQLPDFLGNLQOPRAPRSGLQERAEQVSR 659

Qy      645  LRSALDSC--TSSEAPG 660
Db      660  LQPLADSYFHPGPGTAPG 677

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2006, 11:37:07 ; Search time 199 Seconds
(without alignments)
1548.562 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSWFLSLALGRNPVVVS.....SSEAPGCCCEWDLGPCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: Geneseqp1980s:*
2: Geneseqp1930s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3605	100.0	674	5 AAE14559	Aae14559 Murine cy
2	3583	99.4	698	5 AAE14560	Aae14560 Murine cy
3	3572.5	99.1	683	10 AEF05373	Aef05373 Mouse zcy
4	3569.5	99.0	689	10 AEF05377	Aef05377 Mouse zcy
5	3565	98.9	698	5 AAU11354	AAU11354 Mouse DNA
6	3565	98.9	698	9 AEB55652	Aeb55652 Mouse DCS
7	3562	98.8	698	5 ABB72297	Abb72297 Murine pr
8	3539	98.2	698	5 AAU93161	AAU93161 Mouse int
9	2352.5	65.3	692	4 AAB61880	Aab61880 Human cyt
10	2352.5	65.3	692	5 AAE14562	Aae14562 Human cyt
11	2352.5	65.3	692	7 AEW01911	AEW01911 Human cyt
12	2352.5	65.3	692	10 AEF05349	Aef05349 Human IL1
13	2348.5	65.1	449	10 AEF05374	Aef05374 Mouse zcy
14	2339	64.9	705	4 AAB61884	Aab61884 Chimeric
15	2339	64.9	705	4 AAU29322	AAU29322 Human PRO
16	2339	64.9	705	4 AAB87606	Aab87606 Human PRO
17	2339	64.9	705	4 AAU04956	AAU04956 Human Int
18	2339	64.9	705	5 ABG95931	Abg95931 Human sec
19	2339	64.9	705	5 ABB84998	Abb84998 Human PRO
20	2339	64.9	705	5 ABB95604	Abb95604 Human PRO
21	2339	64.9	705	6 ABU58698	Abu58698 Human ang
22	2339	64.9	705	6 ABU88246	Abu88246 Novel hum
23	2339	64.9	705	6 ABU84561	Abu84561 Human sec

24	2339	64.9	705	6 ABR66435	AbR66435 Human sec
25	2339	64.9	705	6 ABR65825	AbR65825 Human sec
26	2339	64.9	705	6 ABU99765	AbU99765 Human sec
27	2339	64.9	705	6 ABU83004	AbU83004 Human PRO
28	2339	64.9	705	6 ABU90125	AbU90125 Novel hum
29	2339	64.9	705	6 ABR68374	AbR68374 Human sec
30	2339	64.9	705	6 ABU96427	AbU96427 Novel hum
31	2339	64.9	705	6 ABU92858	AbU92858 Human sec
32	2339	64.9	705	6 ABO08935	ABO08935 Human sec
33	2339	64.9	705	6 ABO02987	ABO02987 Human sec
34	2339	64.9	705	6 ABR75141	AbR75141 Human sec
35	2339	64.9	705	6 ABR94903	AbR94903 Human PRO
36	2339	64.9	705	6 ABU85876	AbU85876 Human PRO
37	2339	64.9	705	6 ABU99036	AbU99036 Novel hum
38	2339	64.9	705	6 ABU98251	AbU98251 Novel hum
39	2339	64.9	705	6 ABU91957	AbU91957 Novel hum
40	2339	64.9	705	6 ABU89650	AbU89650 Human PRO
41	2339	64.9	705	6 ABU86491	AbU86491 Human sec
42	2339	64.9	705	6 ABU67704	AbU67704 Human PRO
43	2339	64.9	705	6 ABU80732	AbU80732 Human PRO
44	2339	64.9	705	6 ABU90956	AbU90956 Novel hum
45	2339	64.9	705	6 ABR99650	AbR99650 Human sec

ALIGNMENTS

RESULT 1

AAE14559
ID AAE14559 standard; protein; 674 AA.

XX
AC AAE14559;

XX
DT 17-MAY-2002 (first entry)

XX
DB Murine cytokine receptor, Zcytor14.

XX
KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW gene therapy; protein therapy; receptor.

XX
OS Mus sp.

XX
FH Key Location/Qualifiers

FT Peptide 1..20

FT Protein /label= Signal_peptide

FT Domain 21..674

FT Domain /label= Mature_Zcytor14

FT Domain 21..440

FT Domain /label= Extracellular_domain

FT Domain /note= "Specifically Claimed"

FT Domain 441..461

FT Domain /label= Transmembrane_domain

FT Domain 462..674

FT Domain /label= Intracellular_domain

FT Domain /note= "Specifically Claimed"

WO200204519-A2.

PD 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US021344.

XX 06-JUL-2000; 2000US-0216446P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Zi;

XX WPI; 2002-179701/23.

XX N-PSDB; AAD24220.

XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
PT receptor, useful for treating inflammation, specifically rheumatoid

arthritis, and as educational tools or in research.

Claim 1; Page 90-91; 99pp; English.

The present sequence is murine cytokine receptor, Zcytor14. The Zcytor14 polypeptide is useful for identifying or isolating Zcytor14 ligands, in preparing antibodies, in identifying proteins or peptide cleavage sites, in amino acid sequence analysis, and in monitoring biological activities of both the native and tagged protein in vitro or in vivo. Polypeptides having Zcytor14 activity can be used to treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational tool in genetics, molecular biology, protein chemistry and antibody production analysis, in the preparation of expression constructs for bacterial, viral or mammalian expression, in determining mRNA and DNA localisation of Zcytor14 polynucleotide in tissues, for identifying related polynucleotides and polypeptides by nucleic acid hybridisation, in linkage-based testing for various diseases in murine models, and to determine whether a subject's chromosomes contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo diagnosis, and for detecting and localising Zcytor14 gene expression in tissue samples

Sequence 674 AA;

Query Match 100.0%; Score 3605; DB 5; Length 674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCPLGSLQAPGPV 60
1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCPLGSLQAPGPV 60

61 LVPTRQLTELVRCPKTDKALRVVVHLAVGHWAEPPEEAKGSDSELQESRNASLQ 120
61 LVPTRQLTELVRCPKTDKALRVVVHLAVGHWAEPPEEAKGSDSELQESRNASLQ 120

121 VLVSQAYPIARCALLEVQVADLVPGQSVGSVDFCEASIGAEVQIWSYTKRYQKE 180
121 VLVSQAYPIARCALLEVQVADLVPGQSVGSVDFCEASIGAEVQIWSYTKRYQKE 180

181 LNTQQLPDGNNVLLTLDVSEEDFSLVLRVPDALKSLWYKNTLGPQNTLNTDLV 240
181 LNTQQLPDGNNVLLTLDVSEEDFSLVLRVPDALKSLWYKNTLGPQNTLNTDLV 240

241 PCLCIQVWSLEPDSERVEFCFPREDPGAHNRLWHIARLVRVSPGVQWLDAPCCLPKKVT 300
241 PCLCIQVWSLEPDSERVEFCFPREDPGAHNRLWHIARLVRVSPGVQWLDAPCCLPKKVT 300

301 CWQAPDQSPQPLVPPVPQKNATNEPDQFQVAGHPNLCVQVSTWEKVLQACSWADSL 360
301 CWQAPDQSPQPLVPPVPQKNATNEPDQFQVAGHPNLCVQVSTWEKVLQACSWADSL 360

361 GPFKDDMLLVEMTKGLNNTSVCALEPSGCTPLPSMASTRAAARLGEELLQDFRSHQCWLW 420
361 GPFKDDMLLVEMTKGLNNTSVCALEPSGCTPLPSMASTRAAARLGEELLQDFRSHQCWLW 420

421 NDDNMGSLWACPMKDIHRRVWVWLACLLAALFFLLIKDORRKAAGSRFALLLHS 480
421 NDDNMGSLWACPMKDIHRRVWVWLACLLAALFFLLIKDORRKAAGSRFALLLHS 480

481 ADGAGYERLVGALASALSQMPRLVAVDLWSRRELSAHGALAWFHQRRLIQEGGVILL 540
481 ADGAGYERLVGALASALSQMPRLVAVDLWSRRELSAHGALAWFHQRRLIQEGGVILL 540

541 FSPAAVAQCCQWLQIQTVEPGPHDALAAWLSVLPDFLQGRATGRYGVVFDGLLHPSV 600
541 FSPAAVAQCCQWLQIQTVEPGPHDALAAWLSVLPDFLQGRATGRYGVVFDGLLHPSV 600

601 PSPFRVAFVLSPTQLPAFLDALQGCSTAGRPADRVVTVQALRSALDSCSTSSRAPG 660
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661 CCEWDLGPGCTTLE 674

661 CCEWDLGPGCTTLE 674

RESULT 2

AAEL14560 ID AAE14560 standard; protein; 698 AA.

AAEL14560; AC

17-MAY-2002 (first entry) DT

Murine cytokine receptor Zcytor14 variant, Zcytor14-1. XX

Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis; gene therapy; protein therapy; Zcytor14-1; receptor. XX

Mus sp. OS

Key Location/Qualifiers
Domain 21..464
/label= "Extracellular domain"
/note= "Specifically claimed"

WO200204519-A2. XX

17-JAN-2002. XX

05-JUL-2001; 2001WO-US021344. XX

06-JUL-2000; 2000US-0216446P. XX

(ZYMO) ZYMOGENETICS INC. XX

Gao Z; XX

WPI; 2002-179701/23. XX

N-PSDB; AAD24222. XX

New murine cytokine receptor, Zcytor14, and polynucleotides encoding the receptor, useful for treating inflammation, specifically rheumatoid arthritis, and as educational tools or in research. XX

Claim 1; Page 95-97; 99pp; English. XX

The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14 polypeptide is useful for identifying or isolating Zcytor14 ligands, in preparing antibodies, in identifying proteins or peptide cleavage sites, in amino acid sequence analysis, and in monitoring biological activities of both the native and tagged protein in vitro or in vivo. Polypeptides having Zcytor14 activity can be used to treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational tool in genetics, molecular biology, protein chemistry and antibody production analysis, in the preparation of expression constructs for bacterial, viral or mammalian expression, in determining mRNA and DNA localisation of Zcytor14 polynucleotide in tissues, for identifying related polynucleotides and polypeptides by nucleic acid hybridisation, in linkage-based testing for various diseases in murine models, and to determine whether a subject's chromosomes contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo diagnosis, and for detecting and localising Zcytor14 gene expression in tissue samples. The present sequence is murine Zcytor14 variant, Zcytor14-1 XX

Sequence 698 AA;

Query Match 99.4%; Score 3583; DB 5; Length 698;

Best Local Similarity 96.6%; Pred. No. 0;

Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCPLGSLQAPGPV 60

1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCPLGSLQAPGPV 60

DB

QY 61 LVPTLQTELVLRCPOKTDCAIRVVVHLAVHGHMAEPBEAGKSDSELOESRNASLQAA 120
 DB 61 LVPTLQTELVLRCPOKTDCAIRVVVHLAVHGHMAEPBEAGKSDSELOESRNASLQAA 120
 QY 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 DB 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 QY 181 LNLTLQOLP-----DGNVLLTLDVSEEDFSLLYLRVPD 216
 DB 181 LNLTLQOLPDCGLEVRDSIQSCWVLPWLVNSTDGNVLLTLDVSEEDFSLLYLRVPD 240
 QY 217 ALKSLWYKNTLGPQNTILNHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNLMHIA 276
 DB 241 ALKSLWYKNTLGPQNTILNHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNLMHIA 300
 QY 277 RLRLVSGVWQDAPCCPLPGKVTICWQAPDQSPQPLVPPVQKNATVNEPQDPQLVAGH 336
 DB 301 RLRLVSGVWQDAPCCPLPGKVTICWQAPDQSPQPLVPPVQKNATVNEPQDPQLVAGH 360
 QY 337 PNLVCQVSTWEKVQLOQACSWADSLGPKDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 396
 DB 361 PNLVCQVSTWEKVQLOQACSWADSLGPKDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 420
 QY 397 STRAARLGEELLQDFRSHQCHQWLNDDNMGSLMACPMCKYTHRRWLVWLACLLAAALF 456
 DB 421 STRAARLGEELLQDFRSHQCHQWLNDDNMGSLMACPMCKYTHRRWLVWLACLLAAALF 480
 QY 457 PFLLLKDKRKAARGSTRALLHSGADGAGYERLVGALASALSQMLPRAVDLMSRRLSA 516
 DB 481 PFLLLKDKRKAARGSTRALLHSGADGAGYERLVGALASALSQMLPRAVDLMSRRLSA 540
 QY 517 HGLAWPHHRRRRLQSGGVVILLFSPAQAQCOOVLQOTVEPGRHDAALWLSCVLPD 576
 DB 541 HGLAWPHHRRRRLQSGGVVILLFSPAQAQCOOVLQOTVEPGRHDAALWLSCVLPD 600
 QY 577 FLOGRATGRYGVYDFGLLHPDSVPSPPRVAFLSLPTQLPAFIDLQGGCSTISAGRPAD 636
 DB 601 FLOGRATGRYGVYDFGLLHPDSVPSPPRVAFLSLPTQLPAFIDLQGGCSTISAGRPAD 660
 QY 637 RVERVTQALRSALDSTSSSEAPGCCBEWDLGPTTILE 674
 DB 661 RVERVTQALRSALDSTSSSEAPGCCBEWDLGPTTILE 698

RESULT 3

ABF05373

ID ABF05373 standard; protein; 683 AA.

AC AC

XX AC

XX AC

XX AC

DT 23-FEB-2006 (first entry)

XX AC

XX AC

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10-JUN-2005; 2005WO-US020521.

10-JUN-2004; 2004US-0578805P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;

Jaspers SR, Billsborough J;

WPI; 2006-067457/07.

N-PSDB; ABF05372.

New isolated soluble receptor comprises at least one Zcytor14 subunit,

useful for treating an inflammatory disease, e.g. asthma, inflammatory

bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or

psoriasis.

Disclosure; SEQ ID NO 26; 205pp; English.

The invention describes an isolated soluble receptor comprises at least

one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide

comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises

amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ

ID NO. 24) given in the specification. Also described are: an isolated

soluble receptor comprising Zcytor14, where Zcytor14 comprises a

polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces

the pro-inflammatory activity of either IL-17A comprising fully defined 153

amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153

amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds

to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),

and where the antibody or antibody fragment reduces the pro-inflammatory

activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);

reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal

afflicted with an inflammatory disease in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

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role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

Tue Aug 22 11:34:37 2006

CC	one zcytor14 subunit, where the zcytor14 subunit comprises a polypeptide
CC	comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
CC	amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
CC	ID NO. 24) given in the specification. Also described are: an isolated
CC	soluble receptor comprising zcytor14, where zcytor14 comprises a
CC	polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
CC	the pro-inflammatory activity of either IL-17A comprising fully defined 153
CC	155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
CC	amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
CC	to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
CC	and where the antibody or antibody fragment reduces the pro-inflammatory
CC	activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
CC	reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
CC	afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
CC	role; and treating a pathological condition in a subject associated with
CC	zcytor14 activity. The soluble receptor comprising at least one zcytor14
CC	subunit is useful for treating an inflammatory disease, e.g. asthma,
CC	chronic inflammatory disease selected from inflammatory bowel disease,
CC	ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
CC	psoriasis; or acute inflammatory disease selected from endotoxemia,
CC	septicemia, toxic shock syndrome, or infectious disease. This is the
CC	amino acid sequence of a mouse IL-17A and IL-17F receptor zcytor14
CC	variant.
XX	
XX	Sequence 689 AA;
XX	
XX	Query Match 99.0%; Score 3569.5; DB 10; Length 689;
XX	Best Local Similarity 97.4%; Pred. No. 0;
XX	Matches 671; Conservative 1; Mismatches 2; Indels 15; Gaps 1;
QY	1 MPVSFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSPGPV 60
DB	1 MPVSFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSPGPV 60
QY	61 LVPTRLQTELVRCPQKTDGALRVVVVHLAVGHWAEPPEAGKSDSELSRNASLOAQ 120
DB	61 LVPTRLQTELVRCPQKTDGALRVVVVHLAVGHWAEPPEAGKSDSELSRNASLOAQ 120
QY	121 VVLSFQAPIARCALLEVQVPADLVQFQSVGSVAFDCFEASLGAELVQVSYTPRYOKE 180
DB	121 VVLSFQAPIARCALLEVQVPADLVQFQSVGSVAFDCFEASLGAELVQVSYTPRYOKE 180
QY	181 LNLTOQLP-----DGDVNLTLVDYSEODPSFLLYLRPVPDALKSLWKYN 225
DB	181 LNLTOQLP-----DGDVNLTLVDYSEODPSFLLYLRPVPDALKSLWKYN 240
QY	226 LTGPQNTILNHTDLVPCICIQVWSLEPDSRVEFCPPFREDFGAHRNLWHIARLVLSGV 285
DB	241 LTGPQNTILNHTDLVPCICIQVWSLEPDSRVEFCPPFREDFGAHRNLWHIARLVLSGV 300
QY	286 WQLDAPCCLPKVTLCWQAPDQSPCOPLVPVPQKNATVNEPQDFQVAGHPNLCVQYST 345
DB	301 WQLDAPCCLPKVTLCWQAPDQSPCOPLVPVPQKNATVNEPQDFQVAGHPNLCVQYST 360
QY	346 WEKVQLQACSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSCGCTPLPSMASTRARLGE 405
DB	361 WEKVQLQACSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSCGCTPLPSMASTRARLGE 420
QY	406 ELLQDFRSHQCMQWLNDDNNGSLWACPMQKYIHRRWLVWLAACLLAAALFFFLLLKKDR 465
DB	421 ELLQDFRSHQCMQWLNDDNNGSLWACPMQKYIHRRWLVWLAACLLAAALFFFLLLKKDR 480
QY	466 RKAAGSRRTALLHSADGAGYERLVGALASALSQMPRLVAVDLWSRREL SAHGALAWFHH 525
DB	481 RKAAGSRRTALLHSADGAGYERLVGALASALSQMPRLVAVDLWSRREL SAHGALAWFHH 540
QY	526 QRRRILEGGVILLFSPAAVAQCCQWMLQOTVEPGPHDAAWLSCVLPDFLQGRATGR 585
DB	541 QRRRILEGGVILLFSPAAVAQCCQWMLQOTVEPGPHDAAWLSCVLPDFLQGRATGR 600
QY	586 YVGIVFDGLLHPDSVPSRFRVAFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTOAL 645
DB	601 YVGIVFDGLLHPDSVPSRFRVAFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTOAL 660

QY	352 QACSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSCGCTPLPSMASTRARLGEELLQDF 411
DB	361 QACLWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSCGCTPLPSMASTRARLGEELLQDF 420
QY	412 RSHQCMQWLNDDNNGSLWACPMQKYIHRRWLVWLAACLLAAALFFFLLLKKDRKAARG 471
DB	421 RSHQCMQWLNDDNNGSLWACPMQKYIHRRWLVWLAACLLAAALFFFLLLKKDRKAARG 480
QY	472 SRTALLHSADGAGYERLVGALASALSQMPRLVAVDLWSRREL SAHGALAWFHHQRRIL 531
DB	481 SRTALLHSADGAGYERLVGALASALSQMPRLVAVDLWSRREL SAHGALAWFHHQRRIL 540
QY	532 QEGGVVILLFSPAAVAQCCQWMLQOTVEPGPHDAAWLSCVLPDFLQGRATGRYGVYF 591
DB	541 QEGGVVILLFSPAAVAQCCQWMLQOTVEPGPHDAAWLSCVLPDFLQGRATGRYGVYF 600
QY	592 DGLLHPDSVPSRFRVAFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTOALRSALDS 651
DB	601 DGLLHPDSVPSRFRVAFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTOALRSALDS 660
QY	652 CTSSSEAPGCCBEWDLGPCTTILE 674
DB	661 CTSSSEAPGCCBEWDLGPCTTILE 683

RESULT 4	
AEF05377	
ID	AEF05377 standard; protein; 689 AA.
AC	AEF05377;
XX	
DT	23-FEB-2006 (first entry)
XX	Mouse zcytor14 variant SEQ ID NO 30.
DE	
XX	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
KW	antiarthritic; dermatological; antipsoriatic; antibacterial;
KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
KW	inflammatory bowel disease; asthma; respiratory disease;
KW	ulcerative colitis; antiulcer; Crohn's disease; gastrointestinal-gen.;
KW	gastrointestinal disease; arthritis; antiarthritic;
KW	musculoskeletal disease; psoriasis; atopic dermatitis;
KW	dermatological; immune disorder; atopic dermatitis;
KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;
KW	antibacterial; immunosuppressive; infection; zcytor14; mutein.
XX	
OS	Mus musculus.
XX	
PN	WO2005123778-A2.
XX	
PD	29-DEC-2005.
XX	
XX	10-JUN-2005; 2005WO-US020521.
XX	
XX	10-JUN-2004; 2004US-0578805P.
XX	
XX	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Prenell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
PI	Jaspers SR, Billaborough J;
XX	
XX	WPI; 2006-067457/07.
DR	N-PSDB; AEF05376.
XX	
XX	New isolated soluble receptor comprises at least one zcytor14 subunit,
PT	useful for treating an inflammatory disease, e.g. asthma, inflammatory
PT	bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
PT	psoriasis.
XX	
XX	Disclosure; SEQ ID NO 30; 205pp; English.
XX	
XX	The invention describes an isolated soluble receptor comprises at least
XX	

QY 646 RSALDCTSSSEAPGCCCEWDLGPTCTTLE 674
 DB 661 RSALDCTSSSEAPGCCCEWDLGPTCTTLE 689

RESULT 5
 AAU11354
 ID AAU11354 standard; protein; 698 AA.
 AC AAU11354;
 XX
 XX
 DT 26-MAR-2002 (first entry)
 DE Mouse DNAX cytokine receptor subunit 7 (DCRS7) polypeptide.
 XX
 KW Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling;
 KW gene therapy; protein therapy; immunological disorder.
 XX
 OS Mus musculus.
 XX
 FN WO200190358-A2.
 XX
 XX
 PD N-PSDB; AAS18132.
 XX
 XX
 XX 29-NOV-2001.
 XX
 PP 23-MAY-2001; 2001WO-US016767.
 XX
 XX
 XX 24-MAY-2000; 2000US-0206862P.
 PR
 PA (SCHE) SCHERING CORP.
 XX
 XX Gorman DM;
 PI
 XX WPI; 2002-106198/14.
 DR
 DR N-PSDB; AAS18132.
 XX
 XX
 PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
 PT useful for detecting antibodies generated in response to presence of
 PT increased protein levels or immunological disorders.
 XX
 PS Disclosure; Page 20; 148pp; English.
 XX
 CC The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents the mouse DCRS7 polypeptide
 XX
 SQ Sequence 698 AA;

Query Match 98.9%; Score 3565; DB 5; Length 698;
 Best Local Similarity 96.1%; Pred. No. 0;
 Matches 671; Conservative 1; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTCRSLGLSCHLWDGVDVLCPLGSLQAPGV 60
 DB 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTCRSLGLSCHLWDGVDVLCPLGSLQAPGV 60
 QY 61 LVPTQLQTELVLRCQKTDTCALRVVVVHLVHGHWAEPKGSDELQSRNASLQAO 120
 DB 61 LVPTQLQTELVLRCQKTDTCALRVVVVHLVHGHWAEPKGSDELQSRNASLQAO 120
 QY 121 VVLGFOAYPIARCALLEVQVPADLVQPGQSVGSVDFDCFEASLGAEVQIWSYTKRYOKE 180
 DB 121 VVLGFOAYPIARCALLEVQVPADLVQPGQSVGSVDFDCFEASLGAEVQIWSYTKRYOKE 180

181 LNLTLQQLP-----DGDNVLLTLDVSEEDQSFSLYLRPVPD 216
 DB 181 LNLTLQQLPDCRGLVRDSIQSCWVLPWLVNSTDGDNVLLTLDVSEEDQSFSLYLRPVPD 240
 QY 217 ALKSLWYKNTLGPONITLNTHTDLVPCLCIQWSLEPDSERVEFCPPFDPGAAHNLWHIA 276
 DB 241 ALKSLWYKNTLGPONITLNTHTDLVPCLCIQWSLEPDSERVEFCPPFDPGAAHNLWHIA 300
 QY 277 RLRLVLPFGVWQLDAPCCLPGKVTLCWQAPDQSPQPLVPVPOKNATVNPQDFQLVAGH 336
 DB 301 RLRLVLPFGVWQLDAPCCLPGKVTLCWQAPDQSPQPLVPVPOKNATVNPQDFQLVAGH 360
 QY 337 PNLGVQVSTWVKVQLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPFGCTPLPSMA 396
 DB 361 PNLGVQVSTWVKVQLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPFGCTPLPSMA 420
 QY 397 STFAARLGBELLQDFSHQCMQWLNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALF 456
 DB 421 STFAARLGBELLQDFSHQCMQWLNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALF 480
 QY 457 FFLLLKKDRRKARGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLMSRRLSA 516
 DB 481 FFLLLKKDRRKARGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLMSRRLSA 540
 QY 517 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQMLQQTVEFGPHDALAAMLSCVLPD 576
 DB 541 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQMLQQTVEFGPHDALAAMLSCVLPD 600
 QY 577 FLQGRATGRYGVYFDGLLHPDSVPSFPRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 636
 DB 601 FLQGRATGRYGVYFDGLLHPDSVPSFPRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 660
 QY 637 RVERVTOALRSALDCTSSSEAPGCCCEWDLGPTCTTLE 674
 DB 661 RVERVTOALRSALDCTSSSEAPGCCCEWDLGPTCTTLE 698

RESULT 6
 AEB55652
 ID AEB55652 standard; protein; 698 AA.
 XX
 AC AEB55652;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Mouse DCSR7 polypeptide.
 XX
 KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
 KW DCSR; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
 KW interstitial lung disorder; asthma; allergy; atherosclerosis;
 KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
 KW antipruritic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
 KW antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
 KW IL-17C agonist; mouse; DCSR7; receptor; antisense therapy; RNAi therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 /note= "signal peptide"
 FT Protein 21..698 /note= "mature protein"
 XX
 XX WO2005065711-A2.
 XX
 PD 21-JUL-2005.
 XX
 XX 22-DEC-2004; 2004WO-US042935.
 XX
 PR 29-DEC-2003; 2003US-00749144.
 XX
 PA (SCHE) SCHERING CORP.
 XX

Db 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGAEVQIWSYTKPYQKE 180
Qy 181 LNLITQQLP-----DGDNVLLTLDVSEBQDFSELLYLTPVPD 216
Db 181 LNLITQQLPDCRGLEVRDSTQSCWVLPWLVNSTDGDNVLLTLDVSEBQDFSELLYLTPVPD 240
Qy 217 ALKSLWYKNLTGPQNTILNHTDLVPLCLC:QVMSLEPDSERVFPCPPREDPFGAHRNLWHIA 276
Db 241 ALKSLWYKNLTGPQNTILNHTDLVPLCLC:QVMSLEPDSERVFPCPPREDPFGAHRNLWHIA 300
Qy 277 RLRLVSPGWQLDAPCCLPGKVTLCWQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGH 336
Db 301 RLRLVSPGWQLDAPCCLPGKVTLCWQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGH 360
Qy 337 PNLVQVSTWKEVQLQACSWASGLGPKDDMLLVEMKTLGNNTSVCALESPSGCTPLPSNA 396
Db 361 PNLVQVSTWKEVQLQACSWASGLGPKDDMLLVEMKTLGNNTSVCALESPSGCTPLPSNA 420
Qy 397 STRAARLGBELLQDFRSHQCMQIWNDDNMGSLWACPMCKYIHRRWLVWMLACILLAAALP 456
Db 421 STRAARLGBELLQDFRSHQCMQIWNDDNMGSLWACPMCKYIHRRWLVWMLACILLAAALP 480
Qy 457 PFLLLKKDRKKAARGSRRTALLHSADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSA 516
Db 481 PFLLLKKDRKKAARGSRRTALLHSADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSA 540
Qy 517 HGALAFHHRRIILQEGGVWILLSPAAVQACQWLQIQTVEPGHDAALAWLSCLVPD 576
Db 541 HGALAFHHRRIILQEGGVWILLSPAAVQACQWLQIQTVEPGHDAALAWLSCLVPD 600
Qy 577 FLQGRATGRYGVYFDGLLHPDSVSPFRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 636
Db 601 FLQGRATGRYGVYFDGLLHPDSVSPFRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 660
Qy 637 RVERVTQALRSALDSTSSSEAPGCGEERWDLGPTTLE 674
Db 661 RVERVTQALRSALDSTSSSEAPGCGEERWDLGPTTLE 698

RESULT 8
AAU99161
ID AAU99161 standard; protein; 698 AA.
AC AAU99161;
XX
DT 24-SEP-2002 (first entry)
XX
DE Mouse interleukin 17 receptor like protein, IL-17RL.
KW Mouse; receptor; interleukin 17 receptor-like protein; IL-17RL;
KW chondrocyte; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteoporosis; antirheumatic; antiarthritic; relapsing polychondritis;
KW seronegative spondyloarthritis; bone morphogenetic protein.
XX
OS Mus sp.
XX

Key Location/Qualifiers
FT Key /label= UNKNOWN
FT Misc-difference 627 /note= "Encoded by CSS"
FT Misc-difference 655 /label= UNKNOWN
FT /note= "Encoded by SCG"
FT Misc-difference 668 /label= UNKNOWN
FT /note= "Encoded by SCC"
FT Misc-difference 682 /label= UNKNOWN
FT /note= "Encoded by SCC"
XX

PN WO200238764-A2.
XX 16-MAY-2002.
XX 13-NOV-2001; 2001WO-US043855.
XX 10-NOV-2000; 2000US-0247134P.
PR 23-FEB-2001; 2001US-0271197P.
PR 12-OCT-2001; 2001US-0328904P.
XX (REGC) UNIV CALIFORNIA.
XX Haudenschild D, Rose L, Moseley T, Reddi AH;
PI WPI; 2002-508211/54.
XX N-PSDB; ABR6568.
XX Interleukin-17 receptor-like polypeptide useful for the manufacture of a
PT medicament to modulate cartilage or bone growth in a mammal.
XX Claim 83; Page 89-90; 108pp; English.
XX The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-
CC 17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included
CC are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic
CC host cells, a method of determining the aggressiveness of a prostate
CC cancer cell, by determining the presence or absence in the cell of a
CC group of IL-17RL (where the determination that the group is absent in the
CC cell indicates that the cancer is more aggressive than a like cell in
CC which the group is present) and a mammalian cell comprising a
CC polynucleotide encoding an IL-17B antagonist, where the cell is selected
CC from chondrocyte, synovocyte, and mesenchymal stem cell. IL-17RL or the
CC polynucleotide is useful for the manufacture of a medicament to modulate
CC cartilage or bone growth in a mammal. The polynucleotide is useful for
CC the manufacture of a medicament to restore androgen-responsiveness to a
CC prostate cancer cell. IL-17RL is useful for decreasing catabolic activity
CC in bone or cartilage in a mammal. IL-17RL is useful for inhibiting
CC ossification or calcification in a mammal suffering from pathological
CC ossification or calcification, for diagnosing a cartilage degenerative
CC disorder in a mammal, for inhibiting the rate of proteoglycan synthesis
CC by a chondrocyte in culture, and for the manufacture of a medicament to
CC potentiate the activity of a bone morphogenetic protein in a mammal. An
CC IL-17RL antagonist is useful for treating a bone or cartilage pathology
CC such as a degenerative cartilage disorder selected from osteoarthritis,
CC rheumatoid arthritis, relapsing polychondritis, seronegative
CC spondyloarthropathies, multiple sclerosis, allergic skin immune response
CC and organ transplant rejection. IL-17RL is particularly a receptor for IL
CC -17B (Chondrocyte, a proinflammatory cytokine). The gene for IL-17RL is
CC located on chromosome 3p25.3-3p24.1. The present sequence is the full
CC length sequence for mouse IL-17RL
XX Sequence 698 AA;
SQ

Query Match 98.2%; Score 3539; DB 5; Length 698;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 666; Conservative 1; Mismatches 7; Indels 24; Gaps 1;
Qy 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSGLSGLHWDGVDVLCPLGSLQSPGPV 60
Db 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSGLSGLHWDGVDVLCPLGSLQSPGPV 60
Qy 61 LVPTRLQTELVLRCPOKTDLCALRVVVHVLAVGHWAEPBEACKSDELQESRNASLQAO 120
Db 61 LVPTRLQTELVLRCPOKTDLCALRVVVHVLAVGHWAEPBEACKSDELQESRNASLQAO 120
Qy 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGAEVQIWSYTKPYQKE 180
Db 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGAEVQIWSYTKPYQKE 180
Qy 181 LNLITQQLP-----DGDNVLLTLDVSEBQDFSELLYLTPVPD 216
Db 181 LNLITQQLP-----DGDNVLLTLDVSEBQDFSELLYLTPVPD 216

Db 181 LNLTLQQLPDCRGLEVRDSIQSCWVLPWLVNSTGDGNVLLTLDVSEEQDFSLYLRLPVPD 240
Qy 217 ALKSLWYKNLTPQNTLNHTDLVPCLCIQWLSLEPDSERVEFCPPFRDPGAHRLMHIA 276
Db 241 ALKSLWYKNLTPQNTLNHTDLVPCLCIQWLSLEPDSERVEFCPPFRDPGAHRLMHIA 300
Qy 277 RLRLSPGVQWLDAPCCLPKGVTLQWAPDQSPQPLVPPVPQKNATVNEPQDFQLVAGH 336
Db 301 RLRLSPGVQWLDAPCCLPKGVTLQWAPDQSPQPLVPPVPQKNATVNEPQDFQLVAGH 360
Qy 337 PNLVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGTPPLPSMA 396
Db 361 PNLVQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGTPPLPSMA 420
Qy 397 STRAARLGEELLQDFRSHQWQOLMNDNNGSLWACPMQKTIHRRVWLWLAACLLAAALF 456
Db 421 STRAARLGEELLQDFRSHQWQOLMNDNNGSLWACPMQKTIHRRVWLWLAACLLAAALF 480
Qy 457 FFLILLKDDRRKAAGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLILLKDDRRKAAGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
Qy 517 HGALAWFHQRRIILQEGGVILLFSPAQAQCCQWLQQTVEPGPHDALAAWLSCVLPD 576
Db 541 HGALAWFHQRRIILQEGGVILLFSPAQAQCCQWLQQTVEPGPHDALAAWLSCVLPD 600
Qy 577 FLQGRATGRYGVYDGLLHDPDSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 636
Db 601 FLQGRATGRYGVYDGLLHDPDSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 660
Qy 637 RVERVTQALRSALDSCTSSSEAPGCCSEWDLGPCPTTLE 674
Db 661 RVERVTQALRSALDSCTSSSEAPGCCSEWDLGPCPTTLE 698

RESULT 9

AAB61880
ID AAB61880 standard; protein; 692 AA.
XX AC AAB61880;
XX DT 08-MAY-2001 (first entry)
XX DE Human cytokine receptor Zcytor14.
XX KW Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
XX KW antiinflammatory; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO200104304-A1.
XX PD 18-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018383.
XX PR 07-JUL-1999; 99US-00348854.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Preanell SR, Burkhead SK, Powderer SL;
XX WPI; 2001-112618/12.
XX DR N-PSDB; AAC85027.
XX PT New polypeptide encoding a human cytokine receptor Zcytor14, for treating
XX PS inflammation e.g. rheumatoid arthritis.
XX Claim 2; Page 2; 112pp; English.
XX The invention provides a new human cytokine receptor designated Zcytor14.
XX Zcytor14 can be expressed by standard recombinant methodology. The
XX encoding nucleic acid is useful for detecting the expression of a

CC Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC used to screen biological samples in vitro for the presence of Zcytor14.
CC Proteins, polypeptides and peptides having Zcytor14 activity can be
CC administered to a subject who lacks an adequate amount of this
CC polypeptide, for treating inflammation and conditions such as rheumatoid
CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC antibodies) can be used to treat a subject who produces an excess of
CC Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC Zcytor14 to a subject. The present sequence represents the human cytokine
CC receptor Zcytor14
XX
SQ Sequence 692 AA;
Query Match 65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 2e-216;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;
Qy 1 MPVSWFLSLALGRNPVVVSLERLMEPQDARTCSGLSCHLWDGVLCLPGSLQAPGPV 60
Db 1 MPVSWFLSLALGRNPVVVSLERLMEPQDARTCSGLSCHLWDGVLCLPGSLQAPGPV 60
Qy 61 LVPRLQTELVLRCQKTDCLRVVAVHVAHGHWAEPPE---AGKSDSELQSRNAS 116
Db 61 LVPRLQTELVLRCQKTDCLRVVAVHVAHGHWAEPPE---AGKSDSELQSRNAS 120
Qy 117 LQAOVWLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVFDCFEASLGAEOVWYTKPR 176
Db 121 LQAOVWLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVFDCFEASLGAEOVWYTKPR 180
Qy 177 YQKELNLTQQLP-----DGDNVLTLDVSEHQDFSLYLRLPVPDALKSLWYKNT 227
Db 181 YQKELNLTQQLP-----DGDNVLTLDVSEHQDFSLYLRLPVPDALKSLWYKNT 240
Qy 228 GPQNTLNHTDLVPCLCIQWLSLEPDSERVEFCPPFRDPGAHRLMHIAARLVSPGVWQ 287
Db 241 GPQNTLNHTDLVPCLCIQWLSLEPDSERVEFCPPFRDPGAHRLMHIAARLVSPGVWQ 300
Qy 288 LDAPCCLPGKVTLCWQAPDQSPQPLVPPVPOKNTAVNEPQDFQLVAGHPNLCVOVSTWE 347
Db 301 LDAPCCLPAEALCWAPGGDFCQPLVPPVPSWNTVDKLEFLLKGHPLNCVQVNSSE 360
Qy 348 KVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGCTPLPSMASTAAARLGEEL 407
Db 361 KLQLECLWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSCGCTPLPSMASTAAARLGEEL 420
Qy 408 LQDFRSHQWQOLMNDNNGSLWACPMQKTIHRRVWLWLAACLLAAALFFLLKKDRK 467
Db 421 LQDFRSHQWQOLMNDNNGSLWACPMQKTIHRRVWLWLAACLLAAALFFLLKKDRK 479
Qy 468 AARGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHQR 527
Db 480 AARGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHQR 539
Qy 528 RRILQEGGVILLFSPAQAQCCQWLQQTVEP---GPHDALAAWLSCVLPDFLQGRATG 584
Db 540 RRILQEGGVILLFSPAQAQCCQWLQQTVEP---GPHDALAAWLSCVLPDFLQGRATG 599
Qy 585 RVGVYFDCGLHDPDSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPAVERVTOA 644
Db 600 SYVGACFRLHDPDAVPAVLPVFTVPLPSQLPDLFGALQQPAPRPSRGLQERAEQVSRA 659
Qy 645 LRSALDSC--TSSEAPG 660
Db 660 LQPALDSYFHPFGTPAPG 677
RESULT 10
AAE14562
ID AAE14562 standard; protein; 692 AA.
XX AC AAE14562;
XX DT 17-MAY-2002 (first entry)

XX	Human cytokine receptor Zcytor14.	
DE	Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;	
XX	gene therapy; protein therapy; human; receptor.	
KW		
XX	Homo sapiens.	
OS		
XX	WO200204519-A2.	
PN		
XX	17-JAN-2002.	
PD		
XX		
PF	05-JUL-2001; 2001WO-US021344.	
XX		
PR	06-JUL-2000; 2000US-0216446P.	
XX		
XX	(ZYMO) ZYMOGENETICS INC.	
PA		
XX		
PI	Gao Z;	
XX		
DR	WPI; 2002-179701/23.	
XX		
XX	New murine cytokine receptor, Zcytor14, and polynucleotides encoding the	
PT	receptor, useful for treating inflammation, specifically rheumatoid	
FT	arthritis, and as educational tools or in research.	
PT		
XX		
PS	Disclosure; Page 98-99; 99pp; English.	
XX		
CC	The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14	
CC	polypeptide is useful for identifying or isolating Zcytor14 ligands, in	
CC	preparing antibodies, in identifying proteins or peptide cleavage sites,	
CC	in amino acid sequence analysis, and in monitoring biological activities	
CC	of both the native and tagged protein in vitro or in vivo. Polypeptides	
CC	having Zcytor14 activity can be used to treat inflammation, such as	
CC	rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational	
CC	tool in genetics, molecular biology, protein chemistry and antibody	
CC	production analysis, in the preparation of expression constructs for	
CC	bacterial, viral or mammalian expression, in determining mRNA and DNA	
CC	localisation of Zcytor14 polynucleotide in tissues, for identifying	
CC	related polynucleotides and polypeptides by nucleic acid hybridisation,	
CC	in linkage-based testing for various diseases in murine models, and to	
CC	determine whether a subject's chromosomes contain a mutation in the	
CC	Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo	
CC	diagnosis, and for detecting and localising Zcytor14 gene expression in	
CC	tissue samples. The present sequence is human cytokine receptor, Zcytor14	
CC	which can be used to generate humanised variant of murine Zcytor14	
CC	sequence	
XX		
SQ	Sequence 692 AA;	
	Query Match 65.38; Score 2352.5; DB 5; Length 692;	
	Best Local Similarity 67.48; Pred. No. 2e-216;	
	Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;	
Qy	1 MPVSWFLSLALGRNPVVSLERLMSPQDTRARCSGLSCHLWDGVDVLCPLGSLQSPGPV 60	
Db	1 MPVPWFLLSLALGRSPVVSLERLVGPQDATHCSPLGSLCRMLSDIICLPDGVPAFGPV 60	
Qy	61 LVFRLQTELVLRCQPKTDCLALRVVVVHLAVHGHWAEPPE---ACKSDSEIQESNAS 116	
Db	61 LAPTHLQTELVLRCQKETDCDCLRLVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120	
Qy	117 LQAOVLSFQAYPTARCALLEVQVPADLVQPGQSVGSVAVDCFEASIGASVQVWSYTKPR 176	
Db	121 LQAOVLSFQAYPTARCALLEVQVPADLVQPGQSVGSVAVDCFEALGSEVRVWSYTKPR 180	
Qy	177 YQKEINLTQQLP-----DGNVLLTLDVSEEDQFSLVLRPVPDALKSLWYKNLT 227	
Db	181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEHQFGLSLYWNQVQGPPEKRWKNLT 240	
Qy	228 GPQNTLNHTDLVPLCLCIQVNSLEPDSERVEFCFPREDPGAHRLNWHIARLVLSPGVWQ 287	
Db	241 GPQITLNHTDLVPLCLCIQVWPLEPDSVRTNICFPREDPRAHQVNLWQAARLRLTLQSWL 300	

Qy	288	LDAPCCILPGKVTILCWOAQDOSPCQPLVPPVQKNATVNEPQDFOLVAGHPNLCVQVSTWE	347
Db	301	LDAPCSLPAAALCWRAFGDPCQPLVPPFLSWENVTVDKVLBPFLKAGHPNLCVQVNSSE	360
Qy	348	KVQLQACSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL	407
Db	361	KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYL	420
Qy	408	LQDFRSHQCWQLANDDNMGSWACPMWKYTHRWLVLVWLAACLLLAALFFFLILLKKDRRK	467
Db	421	LQDLQSGGCLQLW-DDDLGALWACPMWKYTHKRWLVWLAACLLFAAALSILLKKDHAK	479
Qy	468	AARGSRFALLHSGADGAGYERLVGALASALSQMPLRVAVDLWSRRRELSAHGALAWFHQR	527
Db	480	AAARGRAALLYSADDSGPERLVGALASALCOLPLRVAVDLWSRRRELSAQGPVAVFWAQR	539
Qy	528	RRILQEGGVILLFSPAANAQCOQWLOLQTVEP---GPHDALAAMLSCVLPDFLQGRATG	584
Db	540	ROTLEGGVVVLLFSPGAVALCSEWLQDGVSGCAHGHDAFRASLSCVLPDFLQGRAPG	599
Qy	585	RYGVVFDGLLHPDSVPSRPAFLPSLTQLPAPFLDALQGGCSTSGRPADEVRYTOA	644
Db	600	SYVGACFDRLLHPDAVPALFRVTVFVTLPSQLPDFLQALQOPRAPRSGRLQERAEQVSR	659
Qy	645	LRSLDSC--TSSSEAPG 660	
Db	660	LQPALDSYFHPGCTPAPG 677	

RESULT 11	
ABW01911	
ID	ABW01911 standard; protein; 692 AA.
XX	AC
ABW01911;	
XX	12-FEB-2004 (first entry)
DT	
XX	Human cytokine receptor Zcytor14.
DE	
XX	Cytokine receptor; Zcytor14; cardiomyopathy; xeroderma pigmentosum;
KW	Marfan-like connective tissue disorder; diabetes mellitus;
KW	Fanconi anaemia; renal cell carcinoma; Marfan syndrome;
KW	Von Hippel-Lindau syndrome; blepharophimosis; human.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide 1..20
FT	/label= Signal_peptide
FT	Protein 21..692
FT	/label= Mature_Zcytor14
FT	Domain 21..452
FT	/label= Extracellular_domain
FT	Domain 453..473
FT	/label= Transmembrane_domain
FT	Domain 474..677
FT	/label= Intracellular_domain
XX	
US2003199041-A1.	
PN	
XX	23-OCT-2003.
PD	
XX	10-JUN-2003; 2003US-00458647.
PF	
XX	07-JUL-1999; 99US-0142555P.
PR	
XX	30-JUN-2000; 2000US-00608918.
XX	
PA	(PRES/) PRESNELL S R.
PA	(BURK/) BURKHED S K.
PA	(POWN/) POWNER S L.
XX	
PI	Presnell SR, Burkhead SK, Pownder SL;

XX	WPI; 2003-852791/79.	RESULT 12	
DR	N-PSDB; RAD47894.	AEF05349	
XX	New zcytor14 polypeptides, useful for treating xeroderma pigmentosum, Marfan-like connective tissue disorder, cardiomyopathy, diabetes mellitus, Fanconi anemia, renal cell carcinoma and Marfan syndrome.	XX	AEF05349 standard; protein; 692 AA.
XX	Claim 1; SEQ ID NO 2; Opp; English.	AC	AEF05349;
XX	The invention relates to human cytokine receptor zcytor14 polypeptide and polynucleotide. The zcytor14 polypeptide, polynucleotide and antibody are useful for treating xeroderma pigmentosum, Marfan-like connective tissue disorder, cardiomyopathy, diabetes mellitus, Fanconi anemia, renal cell carcinoma, Marfan syndrome, Von Hippel-Lindau syndrome, or blepharophimosis. The present sequence is human cytokine receptor zcytor14	XX	23-FEB-2006 (first entry)
XX	Sequence 692 AA;	XX	Human IL17A and F receptor zcytor14 SEQ ID NO 2.
XX	Query Match	XX	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer; antiarthritic; dermatological; antipsoriatic; antibacterial; immunosuppressive; antimicrobial; substrate inhibition; therapeutic; inflammatory bowel disease; asthma; respiratory disease; ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.; gastrointestinal disease; psoriasis; arthritis; antiarthritic; musculoskeletal disease; immune disorder; atopic dermatitis; dermatological; endotoxemia; inflammation; endotox shock; sepsis; antibacterial; immunosuppressive; infection; zcytor14; receptor.
XX	Best Local Similarity 67.4%; Pred. No. 28-216; Indels 19; Gaps 5; Matches 457; Conservative 66; Mismatches 136;	OS	Homo sapiens.
QY	1 MPVSWELLSIALGRNPVVVSLRLEMPQDTARCSLGLCHLWDGVLCLPGSLQAPGV 60	XX	WO2005123778-A2.
Db	1 MPVFWELLSIALGRNPVVVSLRLEMPQDTARCSLGLCHLWDGVLCLPGSLQAPGV 60	XX	29-DEC-2005.
QY	61 LVPTRLQTELVLRCPOKTDCLARVRVVHLAVHGWAEPEE-----AGKSDSLQSRNAS 116	XX	10-JUN-2005; 2005WO-US020521.
Db	61 LAPTHLQTELVLRCQKTDCLARVRVVHLAVHGWAEPEE-----AGKSDSLQSRNAS 120	XX	10-JUN-2004; 2004US-0578805P.
QY	117 LQAVVLSFOAYFIACALLEVQVADLVQPGVSGSAVFDCFEASLGAELVQINSYKPR 176	XX	(ZYMO) ZYMOGENETICS INC.
Db	121 LQAVVLSFOAYFIACALLEVQVADLVQPGVSGVYVDCFEALGSEVRWISYTOPR 180	XX	Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
QY	177 YQKELNLTQQLP-----DGDNVLLTLDVSEQDFSLLYLRVPPDALKSLVKNLT 227	PI	Jaspers SR, Billsborough J;
Db	181 YKELNHTQLPALPWLNVNSADGNVHLVNVSEEHFGLSLYWNQVQPPKPRMHKNT 240	XX	WPI; 2006-067457/07.
QY	228 GPQNTLNHTDLVPCLCIOWSLPESERVEFCPPREDPGAHNLWHIARLRLVLSFGVWQ 287	XX	N-PSDB; AEF05348.
Db	241 GPQITLNHTDLVPCLCIOWSLPESERVEFCPPREDPGAHNLWHIARLRLVLSFGVWQ 300	XX	New isolated soluble receptor comprises at least one Zcytor14 subunit, useful for treating an inflammatory disease, e.g. asthma, inflammatory bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or psoriasis.
QY	288 LDAPCCLPGKVTLCQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGHNLVQVSYWE 347	PS	Claim 7; SEQ ID NO 2; 205pp; English.
Db	301 LDAPCCLPGKVTLCQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGHNLVQVSYWE 360	XX	The invention describes an isolated soluble receptor comprises at least one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ ID NO. 24) given in the specification. Also described are: an isolated soluble receptor comprising Zcytor14, where Zcytor14 comprises a polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces the pro-inflammatory activity of either IL-17A comprising fully defined 153 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153 amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2), and where the antibody or antibody fragment reduces the pro-inflammatory activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16); reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal afflicted with an inflammatory disease in which IL-17A or IL-17F plays a role; and treating a pathological condition in a subject associated with Zcytor14 activity. The soluble receptor comprising at least one Zcytor14 subunit is useful for treating an inflammatory disease, e.g. asthma; chronic inflammatory disease selected from inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or psoriasis; or acute inflammatory disease selected from endotoxemia, septicemia, toxic shock syndrome, or infectious disease. This is the amino acid sequence of human IL-17A and IL-17F receptor zcytor14.
QY	408 LQDFSHOCMLWDDNNGSLWACPMKDYIHRRVVLVWLACLLAAALFFLLKKDRRK 467	CC	Sequence 692 AA;
Db	421 LQDFSHOCMLWDDNNGSLWACPMKDYIHRRVVLVWLACLLAAALFFLLKKDRRK 479	XX	Query Match
QY	468 AARGSRALLHSADGAGYERLVGALASALQMLPRAVDLWSRELSSAGLAWFHQR 527	CC	65.3%; Score 2352.5; DB 10; Length 692;
Db	480 AARGSRALLHSADGAGYERLVGALASALQMLPRAVDLWSRELSSAGLAWFHQR 539	CC	
QY	528 RRLQEGGVVLLFSPFAVAOCQWLQTVPE---GPHDALAAWLSCVLPDFLQGRATG 584	CC	
Db	540 RRLQEGGVVLLFSPFAVAOCQWLQTVPE---GPHDALAAWLSCVLPDFLQGRATG 599	CC	
QY	585 RVGVGVFDGLLPDSVPSPFRVAPLFSPLTQPLPAFLDALQGCSTSAAGPDRVERVTOA 644	CC	
Db	600 SYVGACFDRLHPDAVPALFRTVPVTFPSQLPDLFGLAQPPRPSRGLQERAEQVSRA 659	CC	
QY	645 LRSALDSC--TSSSEAPG 660	CC	
Db	660 LQPALDSYTHPPGTPAPG 677	CC	

Best Local Similarity 67.4%; Pred. No. 2e-216;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLLSALGRNPVVSLSRLMEPQDTARCSLSGLWGDVLCPLGSLQSPGPV 60
DB 1 MPVSWFLLSALGRNPVVSLSRLMEPQDTARCSLSGLWGDVLCPLGSLQSPGPV 60

QY 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEE---AGKSDSELQESRNAS 116
DB 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEE---AGKSDSELQESRNAS 120

QY 117 LQAVVLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPR 176
DB 121 LQAVVLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPR 180

QY 177 YOKELNLTQQLP-----DGNVLLTLDVSEEDQFSLYLRLPVPDALKSLWYKNLT 227
DB 181 YOKELNLTQQLP-----DGNVLLTLDVSEEDQFSLYLRLPVPDALKSLWYKNLT 240

QY 228 GPQNTILNHTDLVPLCLIQVMSLEPDSERVFPCFPREDPGAHRLMWHIARLVLSPGVWQ 287
DB 241 GPQNTILNHTDLVPLCLIQVMSLEPDSERVFPCFPREDPGAHRLMWHIARLVLSPGVWQ 300

QY 288 LDAPCCLPGKVTLCQAPDQSPQPLVPPVPQKNATVNEPQDFOLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPGKVTLCQAPDQSPQPLVPPVPQKNATVNEPQDFOLVAGHPNLCVQVSTWE 360

QY 348 KVOLOQCSWADSLGPPKDDMLVEMKTLNNTSVCALEPSCCTPLPSMASTRARLGEEL 407
DB 361 KVOLOQCSWADSLGPPKDDMLVEMKTLNNTSVCALEPSCCTPLPSMASTRARLGEEL 420

QY 408 LQPRSHQCMLQNDNMGSIMACPMCKYTHRRVVLVLAACLLIAAALFFFLLLKKDRRK 467
DB 421 LQPRSHQCMLQNDNMGSIMACPMCKYTHRRVVLVLAACLLIAAALFFFLLLKKDRRK 479

QY 468 AARGSTFALLHSDAGYERLVGALASASQMPRLRVAVDLWSRRRLSAHGALAWFHQR 527
DB 480 AARGSTFALLHSDAGYERLVGALASASQMPRLRVAVDLWSRRRLSAHGALAWFHQR 539

QY 528 RRILQEGGVVLLSPRAVACQWLOLQVTEP---GPHDAAALVSLCVLPDFLQBRATG 584
DB 540 RRILQEGGVVLLSPRAVACQWLOLQVTEP---GPHDAAALVSLCVLPDFLQBRATG 599

QY 585 RYVGVVFDGLHPDPSVPSRPRVAPLSLPTQLPAFLDALQCGGSTSAGRADRVRVTOA 644
DB 600 RYVGVVFDGLHPDPSVPSRPRVAPLSLPTQLPAFLDALQCGGSTSAGRADRVRVTOA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LRSALDSC--TSSSEAPG 677

RESULT 13
AEF05374
ID AEF05374 standard; protein; 449 AA.

XX AC AEF05374;
XX AC AEF05374;
XX DT 23-FEB-2006 (first entry)
XX DE Mouse zcytor14 extracellular ligand-binding domain.

KW antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
KW antiarthritic; dermatological; antipsoriatic; antibacterial;
KW immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
KW inflammatory bowel disease; asthma; respiratory disease;
KW ulcerative colitis; antiulcer; Crohn's disease; gastrointestinal-gen.;
KW gastrointestinal disease; arthritis; antiarthritic;
KW musculoskeletal disease; psoriasis; antipsoriatic;
KW dermatological disease; immune disorder; atopic dermatitis;
KW dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;
KW antibacterial; immunosuppressive; infection; zcytor14; receptor;
KW ligand binding domain.

XX OS Mus musculus.
XX WO2005123778-A2.
XX PD 29-DEC-2005.
XX PF 10-JUN-2005; 2005WO-US020521.
XX PR 10-JUN-2004; 2004US-0578805P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
PI Jaspers SR, Billeborough J;
XX DR WPI; 2006-067457/07.
XX PT New isolated soluble receptor comprises at least one Zcytor14 subunit,
PT useful for treating an inflammatory disease, e.g. asthma, inflammatory,
PT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
PT psoriasis.
XX PS Disclosure; SEQ ID NO 27; 205pp; English.
XX CC The invention describes an isolated soluble receptor comprises at least
CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
CC ID NO. 24) given in the specification. Also described are: an isolated
CC soluble receptor comprising Zcytor14, where Zcytor14 comprises a
CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
CC the pro-inflammatory activity of either IL-17A comprising fully defined 153
CC amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
CC and where the antibody or antibody fragment reduces the pro-inflammatory
CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
CC role; and treating a pathological condition in a subject associated with
CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
CC subunit is useful for treating an inflammatory disease, e.g. asthma;
CC chronic inflammatory disease selected from inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
CC psoriasis; or acute inflammatory disease selected from endotoxemia,
CC septicemia, toxic shock syndrome, or infectious disease. This is the
CC amino acid sequence of mouse IL-17A and IL-17F receptor zcytor14
CC extracellular ligand-binding domain.
XX SQ Sequence 449 AA;

Query Match 65.1%; Score 2348.5; DB 10; Length 449;
Best Local Similarity 97.6%; Pred. No. 2.4e-216;
Matches 438; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

QY 1 MPVSWFLLSALGRNPVVSLSRLMEPQDTARCSLSGLWGDVLCPLGSLQSPGPV 60
DB 1 MPVSWFLLSALGRNPVVSLSRLMEPQDTARCSLSGLWGDVLCPLGSLQSPGPV 60

QY 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEAGKSDSELQESRNASLQAO 120
DB 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEAGKSDSELQESRNASLQAO 120

QY 121 VLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180
DB 121 VLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180

QY 181 LNLTLQQLP-----DGNVLLTLDVSEEDQFSLYLRLPVPDALKSLWYKNLTGPON 231
DB 181 LNLTLQQLP-----DGNVLLTLDVSEEDQFSLYLRLPVPDALKSLWYKNLTGPON 240

QY 232 ITLNHTDLVPLCLIQVMSLEPDSERVFPCFPREDPGAHRLMWHIARLVLSPGVWQLDAP 291

Db 241 ITLHNTDLVPCLCIQWSLEPDSERFPCPREDPGHRNLWHLRLVLSPGVWQLDAP 300
Qy 292 CCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHPNLCVQVSTWTKVL 351
Db 301 CCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHPNLCVQVSTWTKVL 360
Qy 352 QACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEELLQDF 411
Db 361 QACLWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEELLQDF 420
Qy 412 RSHQCMQLWNDNMGSLWACPMCKYIHR 440
Db 421 RSHQCMQLWNDNMGSLWACPMCKYIHR 449

RESULT 14
AAB61884
ID AAB61884 standard; protein; 705 AA.
XX
AC AAB61884;
XX
DT 08-MAY-2001 (first entry)
XX
DE Chimeric Zcytor14 protein #2.
XX
DE Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antinflammatory; gene therapy; vaccine.
KW
OS Homo sapiens.
XX
PN WO200104304-A1.
XX
PD 18-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018383.
XX
PR 07-JUL-1999; 99US-00348854.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Burkhead SK, Powder SL;
PI WPI; 2001-112618/12.
XX
XX New polypeptide encoding a human cytokine receptor Zcytor14, for treating
PT inflammation e.g. rheumatoid arthritis.
PT
XX
XX Claim 2; Page 105-107; 112pp; English.

XX The invention provides a new human cytokine receptor designated Zcytor14.
XX Zcytor14 can be expressed by standard recombinant methodology. The
XX encoding nucleic acid is useful for detecting the expression of a
XX Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
XX used to screen biological samples in vitro for the presence of Zcytor14.
XX Proteins, polypeptides and peptides having Zcytor14 activity can be
XX administered to a subject who lacks an adequate amount of this
XX polypeptide, for treating inflammation and conditions such as rheumatoid
XX arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
XX antibodies) can be used to treat a subject who produces an excess of
XX Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
XX Zcytor14 to a subject.
XX Zcytor14 protein
XX
SQ Sequence 705 AA;

Query Match 64.9%; Score 2339; DB 4; Length 705;
Best Local Similarity 66.3%; Pred. No. 4e-215;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;
Qy 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCGLSLCHLWDGVLCLPGSLQSPGVPV 60
Db 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCGLSLCHLWDGVLCLPGSLQSPGVPV 60

Qy 61 LVFTRLOTELVLRCPOKTCALRRVVRVHLAVHGHWAPEE-----ACKSDSELQERNAS 116
Db 61 LAPTHLOTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSPGYNAS 120
Qy 117 LOAQVLSFOAYIARCALEVOVPADLVOPGOSVGSVAVDFCFEASLGAEVQWSTYTKPR 176
Db 121 LOAQVLSFOAYIARCALEVOVPADLVOPGOSVGSVAVDFCFEASLGAEVQWSTYTKPR 180
Qy 177 YQELNLTQLP-----DGDNVLTLTLDVSEEQDFSLLYLRPVDPDALKSLWYNLT 227
Db 181 YQELNLTQLPALPWLNVSDGDNVHLVNLVSEEQDFSLLYWNVQVGGPKRWHKNT 240
Qy 228 GPQNTLNHTDLVPCLCIQWSLEPDSERFPCPREDPGHRNLWHLRLVLSPGVWQ 287
Db 241 GPQNTLNHTDLVPCLCIQWSLEPDSERFPCPREDPGHRNLWHLRLVLSPGVWQ 300
Qy 288 LDAPCCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHPNLCVQVSTW 347
Db 301 LDAPCCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHPNLCVQVSTW 360
Qy 348 KVLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KVLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEEL 420
Qy 408 LQDFRSHQCMQLWNDNMGSLWACPMCKYIHRRLVWLACLLLAALFFLLLLKDDRRK 467
Db 421 LQDFRSHQCMQLWNDNMGSLWACPMCKYIHRRLVWLACLLLAALFFLLLLKDDRRK 479
Qy 468 -----AARGSTRALLHSADGAGYERLVGALASALQSMPLRVAVDLWSRRE 513
Db 480 GWRLRLKQDVSRGAAARG-RAALLYSADDSGFERLVGALASALQSMPLRVAVDLWSRRE 538
Qy 514 LSAHGALEWTHQRRLLOEGGVILLIFSPRAVAQCOOVLQVTEP---GPHDALAAML 570
Db 539 LSAQGVANFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGGAHGFHDAPRSL 598
Qy 571 SCVLPDFLQGRATGRYGVYFDGLLHPDSVSPRPAFLPSLPTQLPAFLDALQGCST 630
Db 599 SCVLPDFLQGRATGRYGVYFDGLLHPDSVSPRPAFLPSLPTQLPAFLDALQGCST 658
Qy 631 AGRPADRVERTQALRSALDSC--TSSEAPG 660
Db 659 SGRLQERAEQVSRALQALPDLDSYFHPGTPAGP 690

RESULT 15
AAU29322
ID AAU29322 standard; protein; 705 AA.
XX
AC AAU29322;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #299.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194547P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/58.

N-PSDB; AAS46223.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.

Claim 11; Fig 598; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders

Sequence 705 AA;

Query Match 64.9%; Score 2339; DB 4; Length 705;
 Best Local Similarity 66.3%; Pred. NO. 4e-215;
 Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

QY	1	MPVSWFLLSIALGRNPVNVVSLRLMEPQDARCSTGLSCHLWDGVDVLCPLGSLQSPGPV	60
DB	1	MPVPMFLLSIALGRSPVLSLRLVGVQDATHGCSPLGSLRDLWDSDILCLPGDITVPAPGPV	60
QY	61	LVPTRLQTELRLRCPOKTDCLARVRVVVHLAVHGHWAEPPEE-----AGKSDSELOESRNAS	116
DB	61	LAPTHLQTELRLRCQKETDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS	120
QY	117	LOAQVVLSPQAYPIARFACALLEVQVPADLVQPGQSGVSAVDFCFEASLGAEVQIWSYTKPR	176
DB	121	LOAQVVLSPQAYPTARCVLLEVQVPAALVQFGQSGVSVVYDCFEAALGSEVRISWYTPR	180
QY	177	YQKEINLITQOILP-----DGDNVLLTLDVSEEDQFSLLYLRVPVDALKSLWKNLT	227
DB	181	YEKELNHTQQLPALPMLNVSADGDNVHLVNLVSEEQHFGLSLYMNQVQSGPKPRWHKNLT	240
QY	228	GFQNTITLHNTDLVPCLCIQWLSLEPDSERVEFCPPREDPGAHNLWHIARLRLVSPGVQ	287
DB	241	GFQITITLHNTDLVPCLCIQWLEPDSVRTNCPFPREDFRAHNLWQAARLRLTLQSWL	300
QY	288	LDAPCCLPGKVTLCWQAPDQSPCQPLVPEVPQKNATVNEPQDFQLVAGHPNLCVQVSTWE	347
DB	301	LDAPCCLPAEALCWAPGDFCQPLVPLSWENVTVDKLEFPFLKGFENLCVQVNSSE	360
QY	348	KVQLQACSWADSLGPFKDDMLLVEMKMTGLNNTSVCALEPSGCTPLPSMASTRARLGEEL	407
DB	361	KLQLECLWADSLGPLKODVLLLETRGPQDNRSCLALEPSGCTSLSPSKASTRAARLGEYL	420
QY	408	LODFESHOCWOLWDDNMGSLWACPMDKYIHRWLVWLACLLLAALFFFLKKDRK	467
DB	421	LQDLSGQCQLW-DDDLGLWACPMDKYIHRWLVWLACLLFAAALSILLLKKDHAK	479
QY	468	-----AAGSRTALLHSADGAGVERLVGALASALSQMLRVAVDLWSRRE	513
DB	480	GWLRLKKQDVRSGAAARG-RAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRE	538
QY	514	LSAHGALAWFHRRRIQEGGVILLFSPAAVAQCOQWLQQTVEP---GPHDAAWL	570
DB	539	LSAQGFVAWFHAQRRTLQEGGVVLLFSPGVALCSEWLQDGVSGFAGHPHDAFRASL	598
QY	571	SCVLPDFLOGRATGRVGVYVFDLLHPDSVPSFPRVAPLPSLPTQLPAFLDALOGGCGSTS	630
DB	599	SCVLPDFLOGRAPGSYVGACFDRLLHPDAVPALFTVPVFTLPSQLPDLFGLALQOPRAPR	658
QY	631	AGRPADRVERTQALRSALDSC--TSSSEAPG 660	
DB	659	SGRLQERAEQVSRALQPALDSYFHPFGTPAG 690	

Search completed: August 16, 2006, 11:40:56

Job time : 204 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:41:17 ; Search time 44 Seconds
(without alignments)
1473.866 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSWFLSLALGRNPVVS.....SSEAPGCCSEWDLPCTTLE 674
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	3.2	267	2 A38442	probable tumor sup
2	114.5	3.2	1013	2 B70841	probable helz prot
3	110	3.1	2910	2 T42214	ocogelin - mouse
4	108.5	3.0	361	2 T39784	hypothetical prote
5	106.5	3.0	478	2 D75564	hypothetical prote
6	105.5	2.9	698	2 A82593	hypothetical prote
7	105.5	2.9	1451	2 B41185	alpha-2 macroglobu
8	105	2.9	1615	2 B49502	protein-tyrosine-p
9	105	2.9	1767	2 A49502	protein-tyrosine-p
10	103.5	2.9	3707	2 S18252	heparan sulfate pr
11	103	2.9	851	2 T31520	hypothetical prote
12	103	2.9	906	2 G83156	probable transcrip
13	102.5	2.8	1711	1 A55148	protein-tyrosine-p
14	101.5	2.8	1476	2 A41185	alpha-2 macroglobu
15	100	2.8	1447	2 A54100	tumor suppressor p
16	99.5	2.8	2647	2 A37098	gelation factor AB
17	99	2.7	1617	2 T28153	complement C4 - ch
18	99	2.7	2437	2 S42612	transmembrane prot
19	99	2.7	3014	1 JC5620	genome polyprotein
20	98.5	2.7	665	2 S69222	probable transcrip
21	98	2.7	824	2 H85498	helicase, ATP-depe
22	98	2.7	824	2 H90647	ATP-dependent heli
23	97.5	2.7	1618	2 S21424	nestin - human
24	97.5	2.7	1763	2 T17465	rifamycin polyketi
25	97.5	2.7	1894	2 C54689	protein-tyrosine-p
26	97.5	2.7	2629	2 T30987	telomerase-associat
27	97	2.7	604	2 G83091	conserved hypothet
28	97	2.7	963	2 T09478	ubiquitin thiolest
29	96.5	2.7	813	2 AF0526	ATP-dependent heli

30	96.5	2.7	1187	2 JE0347	hypothetical prote
31	96.5	2.7	1691	1 D54689	protein-tyrosine-p
32	96.5	2.7	2535	2 T04824	hypothetical prote
33	96	2.7	564	2 D96017	probable peptidase
34	95	2.6	1573	2 S01845	DNA (cytosine-5')-
35	95	2.6	10223	2 T30225	polyketide synthas
36	94.5	2.6	445	2 E70854	probable membrane
37	94.5	2.6	837	2 A34898	granulocyte colony
38	94.5	2.6	6260	2 T30228	polyketide synthas
39	94	2.6	509	2 JC5288	SHP substrate-1 pr
40	94	2.6	513	2 JC5289	SHP substrate-1 pr
41	93.5	2.6	527	2 A48085	transcription fact
42	93.5	2.6	1513	2 T23681	hypothetical prote
43	93.5	2.6	6831	2 A88852	protein unc-22 [im
44	93.5	2.6	6839	2 S57242	twichin [similari
45	93.5	2.6	7160	2 T27935	hypothetical prote

ALIGNMENTS

RESULT 1

A38442
probable tumor suppressor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Feb-1997
C:Accession: A38442
R:Nigro, J.M.; Cho, K.R.; Fearon, E.R.; Kern, S.E.; Ruppert, J.M.; Oliner, J.D.; Kinzler
Cell 64, 607-613, 1991
A:Title: Scrambled exons.
A:Reference number: A38442; MUID:91121517; PMID:1991322
A:Accession: A38442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 -NIG>

A:Cross-references: UNIPARC:UPI000017C31D; GB:M63696; GB:M63700; GB:M63702; GB:M63718; GE
C:Keywords: transmembrane protein

Query Match 3.2%; Score 116; DB 2; Length 267;
Best Local Similarity 25.6%; Pred. No. 0.14;
Matches 72; Conservative 31; Mismatches 100; Indels 78; Gaps 16;

QY	155	VDFCFEASIGAEVQISYTKPRYQKELNLTOQLPD-----GDNVLLTLDVSEQDFSL 209
DB	8	LYQC-EASLGDGSGSIISRTAKVAVAPLRPLSQTESVAFMGDTVLKCEVGE-----59
QY	210	YLRVPDALKSLWYNLTGPNITLNHTD-----LVPLCLIQVWSLEPDSERVEFCFPRED 265
DB	60	---PMFTI---HWQKN---QQDLTPGDSRVVVLPSGALQISRLQPGDIGYRCSAR-N 109
QY	266	PGAHRLNHLRLVLSPCVMOLDAPCCLPKGVTLQWQAPD-QSPCQPLVPPVP-----OK 320
DB	110	PASSRT-GNEAEVRILSP-PWFLNHPNL-----YAYESMDIEFFECTVSGKVPVTNNWK 162
QY	321	NATVNEPQDFQIVAGHPNLQVQVSTWEKVLQACSWADSLGPPFKD-----MLIVENKTGL 376
DB	163	NGDVVIPSDFQIVGSGNLRI-----LGVKSDGEGFYQCVAEAGN 204
QY	377	NNTSVCALEPSGCTPLPS-----MASTRAARL 403
DB	205	AQTSQAQLIVPK---DIPSSSVLPSPAPRDVVPVLVSSRFVRL 242

RESULT 2

B70841
probable helz protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: B70841
R:Coile, S.I.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70841
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1013 <COL>
A;Cross-references: UNIPROT:O53499; UNIPARC:UPI00000D7368; GB:AL021924; GB:AL123456; NID:
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: heiz

Query Match		3.2%;	Score 114.5;	DB 2;	Length 1013;
Best Local Similarity		20.4%;	Pred. No. 0.97;		
Matches		143;	Conservative 75;	Mismatches 232;	Indels 251; Gaps 33;
QY	90	LAVHGHWAEP--EEAGKSGSELOESRNASLOAQVLSFOAVPIARCALLEVQVADL---	144		
DB	2	LVLHGFSNSGMRUWADSLL-----VKSPQALRSARPHFA-----APADLIAG	49		
QY	145	VQPGSVGSVAFDCFEASIGAEVQIWSYTKPRYQKELNLTQOLPDGDNVLLTLDVSEQD	204		
DB	50	IHPGK-----PATAVLLLPSSLSAPLD	71		
QY	205	FSFLYLPRVPDALKSLMYKNLTGPQNTILNHTD-LVPCLCIQWSLEPDSEVFECFPR	263		
DB	72	SPELIRLAPRAA-----RTDPMLLAWTPVVVDLDPATAALAFDQPA	113		
QY	264	EDPGAHRNLWHIARLVLSPGVWQLDAPCLPGKV-----TLGW-----QAPQOS	308		
DB	114	PDVRYGASVYLAELAVARELVE-----RGRVLPQLRDTHGAACWRPVLOGRDV	166		
QY	309	PCQPLV---PPVPQKNATVNEPDQFLVA-----GHPNLCVQ	342		
DB	167	AMTSLVSAMPPVCAEVGCHDPHELATSALDAMVDAVAEALSPMDLLPRRGRSKHRA	226		
QY	343	VSTW-----EKVQLOACS-----WAD-----SLGPFKDDMLLVEMKTLNNTS	380		
DB	227	VEAMLTALTCPDGRFDEPDELDAEALRPMDVVGIGTGVGPARTFRLSEVETENEET-	285		
QY	381	VCALPSPGCTPLPSPMASTRAARLGBELLDQFRSHQW---OLWDDNMGSLWACPMDKY	436		
DB	286	-----PAG-----SLWRL-FLQLQSTQDPSLLVPAEQAWND--GSL-----	319		
QY	437	THRRVW---LVWLACLLAAALFFLLKKDORRKAAGSRTPALLHSADGAGYERLVCA	492		
DB	320	--RWLDRPQELLTELGRASRIFPELV-----PALRTACPSGLELDADGA--YRFLSG	369		
QY	493	LASALSQMLRVAVDLWSRELSAHGALAWPHHRRITLQEGGVILLFSP--AAVAQCQ	550		
DB	370	TAAVLDEAGFGVLLPSW-----W-----DRRRKL---GLVLSATYPVDGVVVGKAS	411		
QY	551	OWLQQTVE-----PGPHDALAAWLSVLP-----DFLQG	580		
DB	412	KGRQLVEFRWELAVGDDPLSEEEIALTETKSPILRLRGQWVALDTEQMRGLEFLER	471		
QY	581	RATGRVGVYFGLL--HPDSVPSFRVAPLSLTQLPAFLDALOGGSGTSAGRAPADV	638		
DB	472	KPTGRKTTAEILALAAASHPDDVDTPLETAV-----RADWGLGDLIAGAAAALQFLDPP	526		
QY	639	ERVTOALRSALDSCIS-----SSEAPGCCCEWDLGPGCTTLE	674		
DB	527	DGFTATLRPYQQRGLAWLAFSLSLGSLGSLADMDMLGKTVQ	567		

RESULT 3
T42214
ocogelin - mouse
N;Alternate names: mucin-like extracellular matrix protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T42214
R;Cohen-Salmon, M.; El-Amraoui, A.; Leibovici, M.; Petit, C.

Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A;Title: Ocogelin: A glycoprotein specific to the acellular membranes of the inner ear.
A;Reference number: Z22079; MUID:98070772; PMID:9405633
A;Accession: T42214
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-2910 <COH>
A;Cross-references: UNIPROT:O52225; UNIPARC:UPI0000027C49; EMBL:U96411; NID:G2760883; PII
A;Experimental source: strain BALB/c
A;Note: Component of all the acellular membranes of the inner ear
C;Superfamily: von Willebrand factor

Query Match		3.1%;	Score 110;	DB 2;	Length 2910;
Best Local Similarity		20.8%;	Pred. No. 8.4;		
Matches		54;	Conservative 31;	Mismatches 82;	Indels 92; Gaps 13;
QY	214	VPDALKSLMYKNLGTGPQNTILNHTDLVPCLCIQWSLEPDS-----ERVFCFPR	263		
DB	2427	VPRALGETWNSLSG-----CCQCCQAPDTIIPVDLDCPGPRPESCP--	2469		
QY	264	EDPGAHRNLWHIARLVLSPGVWQLDAPCLPGKVTLCWQAPDQSPCQPLVPPVQKNAT	323		
DB	2470	-----RFGEVILLQP-----TEDPCCL-GSVCVC---NQTLCGLAPTCPGSHSL	2510		
QY	324	VNEPDQFLVAGH-----PNLCVQVSTWEKVQLOACSWSADSLGPPKDDMLLVEMKTLN	378		
DB	2511	ITHFQEDSCCPSYSCEDPGLC-----EASQVPTC-----REQILLIEGRLG---	2552		
QY	379	TSVCALEPSGC---TPLPSPMASTRA-----ARLGEELQDFRSHQ-----	415		
DB	2553	DSCCTSYFCGCEGSDPMECEQEGEALTVRHTTTELCCLPQVCENFCRCQVQCGMETS	2612		
QY	416	CMQLWDDNMGSLWACPMD	434		
DB	2613	LVEVMSPDRCPCPKSCECD	2631		

RESULT 4
T39784
hypothetical protein SPBC18H10.20c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39784
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21879
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-361 <LYN>
A;Cross-references: UNIPROT:O60150; UNIPARC:UPI000006A75B; EMBL:AL022304; PIDN:CAA18417.1
A;Experimental source: strain 972h; cosmid c18H10
C;Genetics:
A;Gene: SPDB:SPBC18H10.20c
A;Map position: 2

Query Match		3.0%;	Score 108.5;	DB 2;	Length 361;
Best Local Similarity		20.3%;	Pred. No. 0.79;		
Matches		84;	Conservative 53;	Mismatches 133;	Indels 143; Gaps 21;
QY	16	PVVVSLERLMEPQDTARCSLGLSCHLWDGDLVCLPGSLQSAFG-----PVL	61		
DB	2	FLKALPRSTTPKDPARCTDIR--MESPPVLVFLGSPETSSGALASGILKLTILHQPFI	58		
QY	62	VPTRLQTELVLRCPOKTDICALRVVVHLAVGHWAEPPEACKSDELSERNASLOAQV	121		
DB	59	KVHTLKLQLIKRI-----TVLHPAI-SHCS-----ACAGSKEVLTQWDLAANTTY	102		
QY	122	VLSFOAYPIARCALLEVQVADLVQPGQSVGAVDFCFEASIGAEVQIWSYTKPRYQKEL	181		
DB	103	RGTOHQWPPSW-----LFFGSLPASVSN-RYIKLEYLEA	136		
QY	182	NLTQQLPDGDNVLLTLDVSEBQDFSFLLYL---	237		

QY 621 DALGGGSTSAGRPADRRVRYVTQALRSAL 649
DB 400 VFPLGPDPLEVRLPCDRLTLTRPDYRAEL 428

RESULT 6
A82593
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: A82593
R/anonymous: The xylella fastidiosa Consortium of the Organization for Nucleotide Sequen-
A/Nature 406, 151-157, 2000
A/A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/A/Reference number: A82515; MUID:20365717; PMID:10910347
A/A/Note: for a complete list of authors see reference number A59328 below
A/A/Accession: A82593
A/A/Status: preliminary
A/A/Molecule type: DNA
A/A/Molecule type: DNA
A/A/Residues: 1-698 <STM>
A/A/Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NID
A/A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A-
Brigues, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrez, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm-
J.D.; Junqueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr-
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miraccca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.; Z-
A/Reference number: A59328
A/Contents: annotation

[illegible]

Db 466 AAIAPAEILARPELL-----INGPGSHVERVTMMWASSMLC----- 502
Qy 456 FFFLLKKDRKAARGSTALLHSADGAGYERLVGLASALSOMPLURVAVDLWSRRELS 515
Db 503 -----ADRYSETP-----PADPLQRYETVSELTS--GTLTPQALIDAW--ROQLP 543
Qy 516 AHGA-----LAWFHQ-----RRRILOEGGVILLSPRAVAQCQCQWLQTVPEQPH 563
Db 544 ARGIEDGNVIDWLLWMDNSLITATLPHLPEGRLLIIVLRDPRDM--LLDWIAYGSPILAL 601
Qy 564 DAL-----AAWLSVLPDFQGRATGRYGVYDGLLHPDSV--PSPFRVA-----PLFSLPTQ 615
Db 602 DSLQQAANWLG-----DILNQIAALHELDLYPHLIRLDGIEDNPQALATTLEDIFGSPFP 657
Qy 616 LPAFIDALQGGCSTAGRAPRVERVTOALRSALDS 651
Db 658 IPPSLEAPR-----LPAGRWRDYREVLSAPDA 685
RESULT 7
B41185
alpha-2 macroglobulin homolog MUC2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text change 09-Jul-2004
C:Accession: B41185
R:Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A:Title: Molecular characterization of the murinoglobulins.
A:Reference number: A41185; MUID:91358495; PMID:1840592
A:Accession: B41185
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1451 <OVS>
A:Cross-references: UNIPROT:P28666; UNIPARC:UPI0000028B3F; GB:M65238; NID:g199888; PIDN:
C:Superfamily: alpha-2-macroglobulin
Query Match 2.9%; Score 105.5; DB 2; Length 1451;
Best Local Similarity 20.4%; Pred. No. 7.9;
Matches 76; Conservative 48; Mismatches 159; Indels 89; Gaps 17;
Qy 67 QTELVRCPQ-----KTDICALRVVVVHLV-----HGHWAEPREA--- 102
Db 454 ETSSILPCNQIHTVQAHFTLKGLGVLKELVLYLVMAQSIITQGNHTHVEPGEAPVK 513
Qy 103 GKSDSELOESRNASLOAQVVLSPQAYPIARCALLEVQVPADLVQPGQSVGSVDFCFEAS 162
Db 514 GNFDLE-----IPVEFSMAPMAKMLIYVILPDGEVI--ADSVNFEIEKCLRNK 559
Qy 163 LGAEVQIWSYTKPRYQKELNLTQOLPDGNDVLTLDVSEEDFSFLLYLRPVPDALKSLW 222
Db 560 VDLFSFS--SQSLPASQTRLOVTAS--PQSLCGLRAVDQS-----VLLKLP--EDELSPSW 609
Qy 223 YKULTGQNTLTHDVLV-----CLCIQVWSLEPDSERVFPCPPREDPGAHR-- 270
Db 610 IYNLPQMQ-----HNKFIPISSLSSEDDCILVSSWAE---KHTDWVHGKEDVYRV 661
Qy 271 ---NLWHIARLRLVSPGWQLDAPCCLP--GKVTLCWQAPDQSPQ-----PLVPPVPQK 320
Db 662 EDMDLKAFNTLKIKLPKICFDSAPMSGPRGKFDLAFSEVSGTILQKGSRRKRPQPEPPRE 721
Qy 321 NATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWA-----DSLGPFKDDMLLVEMK 373
Db 722 DPPPDKPLAETIRKYFFETWY----WDIVTVNSTGVAEVEMTVPTDITTEWAGALCLNSD 777
Qy 374 TGLNNTSVCALE 385
Db 778 TGLGLSSVWPLQ 789
RESULT 8
B49502
protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type 4E, splice form B precursor - f

C:Species: Drosophila melanogaster
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: B49502
R:Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A:Title: Alternative splicing in a novel tyrosine phosphatase gene (DPTP4E) of Drosophila
A:Reference number: A49502; MUID:94043220; PMID:8226938
A:Accession: B49502
A:Molecule type: mRNA
A:Residues: 1-1615 <OON>
A:Cross-references: UNIPROT:Q9W4F5; UNIPARC:UPI0000177053; GB:L20894
C:Genetics:
A:Gene: FlyBase:Pcp4E
A:Cross-references: FlyBase:FBgn0004368
A:Introns: 1605/3
C:Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repeat
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor
F:1254-1270/Domain: transmembrane #status predicted <TMN>
F:1271-1615/Domain: intracellular #status predicted <INT>
F:1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1531/Binding site: substrate phosphate (Arg) #status predicted
Query Match 2.9%; Score 105; DB 2; Length 1615;
Best Local Similarity 22.3%; Pred. No. 9.9;
Matches 98; Conservative 49; Mismatches 136; Indels 156; Gaps 26;
Qy 60 VLVPTRLQTELVLRC-----PQKTDICALRVVVVHL-----AVGHWAEPREA 102
Db 403 ILEPGRTY-EVVVKTADNVNVPASGEVTLRPRVPSLGGFLDDRSNALHISM-EPAPT 460
Qy 103 GKSDS---ELOESRNAS-----LQAOVVLSPQAYPI-----ARCALEVQVPADLV 145
Db 461 GRQDSYRISYHEQTNWASEVPAPVPAESQITNLTETLDSLLAGRYLIAVQALS--- 517
Qy 146 QPGQSVGSVDFCFEASLGAEVQIWSYTKPRYQKELNLTQOLPDGNDVLT---TLDVSEE 202
Db 518 ---KGVASNASD-----ITRYTRP-----AAPLIQELRSIDQGLMLSWRSDVNSR 559
Qy 203 QD-----PSFLLYLRP-----VPDALKSLWYKNLTG-- 228
Db 560 QDRYEVHYORNGTRERTWATNETSLTTHYLPGSGYEVKVAISHGVRSBHSYFQAVF 619
Qy 229 ---PQNIITLN--HTDLVPCLCIQVWSLEPDSF-----RVFPCFFREDPGAHRN--- 271
Db 620 PKPPQNLITQTVHTNLV---VLHWQAPEGSDFSEYVVRVYRTDASFPQWRISGLHENEARI 675
Qy 272 -----LWHIARLRLVSPGWQLDAPCCLP--GKVTLCWQAPDQSPQPLVPPVPQKNATVN 325
Db 676 KDMHYGERYLQVNTVSGV---ESPHPLELNVTM-----PPQ-PVSNVVPLVDSRNLITLE 727
Qy 326 EPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMK--TGLNNTSVCA 383
Db 728 WRP-----DGH-----VDFYTLKWPT-----DEEDRVEFKNVTQLEDLS--- 763
Qy 384 LEPSCGTPLPMSASTRAAR 402
Db 764 -SPSVRIPIEDLSPGQYR 781
RESULT 9
A49502
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor -
C:Species: Drosophila melanogaster
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C:Accession: A49502
R:Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A:Title: Alternative splicing in a novel tyrosine phosphatase gene (DPTP4E) of Drosophila
A:Reference number: A49502; MUID:94043220; PMID:8226938
A:Accession: A49502
A:Molecule type: mRNA
A:Residues: 1-1767 <OON>

A;Cross-references: UNIPARC:UPI0000016CFA0; GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:
A;Accession: B31917
A:Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: UNIPARC:UPI0000016CPA8; GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:
R;Schulze, B.; Mann, K.; Battisututta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A:Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
A;Cross-references: UNIPARC:UPI0000017C67C
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGP>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.9%; Score 103.5; DB 2; Length 3707;
Best Local Similarity 20.5%; Pred. No. 37; Mismatches 167; Indels 127; Gaps 19;
Matches 87; Conservative 44;

	QY	DB	
	26	EPDPTARCSLQ-LSCHLW--DGDVLCPLGSLQS-----APGPVLVPTRLTQLTELVLRL---	73
	326	EPNEFA-CENGHCALKLRCDGDFDCEDRTDEANCSVKQPGEVCQTHFCQCVSTNRICIPA	384
	74	---CPQKTDICALRVVVVHLAVGHWAEBPEBAGKSDSBELQSRNASLQAQVVLVSFOAYPI	130
	385	SFHCDSESDCPDR-----SDEFGCMPQPQVTPPPQSIQA-----	418
	131	ARCALLEVQPADLVQPGSQSVGSVAFFDCFASISLGAENVQIWSYTKPRYQKELNLTLQOLPDG	190
	419	-----SRGTQV---TFTCVATGVPTPIINRWLNWGHIPAHPRVTMTSEG	460
	191	DNVLLTLDVSEEQDFSLLL-----YLRPVPDALKSLWKNLITGPQN---ITLNHTDLVP	241
	461	RGTLIIRDVKEADQGATCTEAMNSRGWVGFGIDGVLELPVRGPGCPDGHFYLEDSASCILP	520
	242	CLCIQVMSLEPDSERVEFPREDPGAHRNLWHIARLRVLSFGVMQLDAPCCPLG-KVTL	300
	521	CFCFGVTNVQSSSLR-----FRD-----QIRL-----SFDPDNDFKGVNVTM	557
	301	CWAQPDSPQCPPLVPVPQKNATWNEP-QDFQLVAGHPNLVCVOVSTWEKVQLOACSWADS	359
	558	-----PSQGGPVVLSSTQLQIDPALQEFLVDLSRRPLVHDAPFWALPKQFLGNKVDS	609
	360	LGPFKDDMLIAEMKTGLNNITSVCALEP-----SGCTPL-PSMASTRAA	401
	610	YGGLRYKYRYELARGM-----LEPVQPDVILVGAGYRLHSRGHPTTPTGTLNQORV	662
	402	RLGEE 406	
	663	QLSEE 667	

RESULT 11
T31520
hypothetical protein Yll6A8C.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 23-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
R;McMurray, A.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21041

A;Accession: T31520
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
A;Cross-references: UNIPROT:Q9U2S3; UNIPARC:UPI000008020F; EMBL:AL117204; PIDN:CAB55154.
A;Experimental source: Clone Y116A8C
C;Genetics:
A;Gene: CESP:Y116A8C.14
A;Introns: 99/3; 124/2; 193/2; 225/3; 431/3; 660/2; 709/1; 795/3

Query Match 2.9%; Score 103; DB 2; Length 851;
Best Local Similarity 19.7%; Pred. No. 6.4; Indels 188; Gaps 34;
Matches 114; Conservative 88; Mismatches 88

QY 103 GKSDSELOESRNASLQAQVLSF-----QAYPIARCALLEVQVPAD 143
DB 41 GKNQLFFSAARHSIEATEPLFSNEEDAEKGRALPTWASIKRARGQPKTSVGNQIILYD 100
QY 144 -LVQP-GQSVGSAVDFCEASLGAEOVWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSE 201
DB 101 TLQPQRESIPSAIFNSFS-----NLKKGTPVSKRVNF----- 135
QY 202 EQDFSFLLVLRVPDALKSLWKNLGTQNTILNHTDLVPCLCIQWMSLEPDSERVEFCP 261
DB 136 QKSFRAKCKLRISWVA-----YAVN-----TIEHPDEA-----SLOPETDSMEVKP 176
QY 262 FREDFGAHLNWHIARLRVLSFGVWQLDAPCCLPKGVTLCWQAPDQSPQCLVPPVPQKN 321
DB 177 ILENFENRRRIGVL--FSYLLP-VFNI-----LPSKTQ---QAPPRTLINSIPLTSKQK 225
QY 322 ATVNPDPQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPKFDDMLLVEMKTLGLNNTSV 381
DB 226 PSLRSLSURL-----PDFSTER-FDFDKHNSCS-PDNVQPEE----- 262
QY 382 CALEPSCGCTPLPSMASTRAARLGEELLQDF--RSHQCMQLMNDNMGSLWACPMKYI-- 437
DB 263 --LAPSKITPFIKHCAR-----EELTRKFARKVHDKIRVK---ANLWS-KTDQFLAM 310
QY 438 ---HRRWLVWLA-----CLLLAAALFFLLLKDDRRKAARG-----SRTALLLHS 480
DB 311 GVDERPWFYTWISTVQTFVCIL--SLLFYGFAPPALEMEAREAGDVMDITLSSRRVAYLEQ 368
QY 481 AD---GAGYERLV--GALASALSQMLPRVAVDLWSRRELSAHGALAWFHHRRILOEGG 535
DB 369 SNPWFPGHYADLIRLGAVSPC---MRRELEMWKAE-----EURLIENKTG 412
QY 536 VVTL-----LFSFAAQQCOQLQLOTFEPG-----PHDALAAWLSCLVLPDFLQ 580
DB 413 CCITNDRSGCYQSSSICPRTMARWIRWDKPLTAASKNFLTHTSKTIW-----TOP 464
QY 581 RATGRVGVVFDGLLHPDSVPSFRVAPLPSLP---TQLP 617
DB 465 RKSGAVCG-----QDPYSYCRPLSVAP-YEWPDDSTQMP 497

RESULT 12
G83156
probable transcription regulator PA3921 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83156
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83156
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-906 <SRO>
A;Cross-references: UNIPROT:Q9HX92; UNIPARC:UPI000000CSB79; GB:AE004809; GB:AE004091; NID
A;Experimental source: strain PAO1

C;Genetics:
A;Gene: PA3921
C;Superfamily: regulatory protein malt

Query Match 2.9%; Score 103; DB 2; Length 906;
Best Local Similarity 20.7%; Pred. No. 6.9;
Matches 97; Conservative 45; Mismatches 136; Indels 190; Gaps 23;

QY 313 LVPPVPQKNATVNEPDPQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPKFDDMLLVEM 372
DB 348 LARELP-----DFGPSAG-----SUHLRACGWFRRHG-----LDDQ 378
QY 373 KTGLNNTSVCALEPSCGCTPLPSMASTRAARLGEELLQDFRSHQCMQLMNDNMGSLWACP 432
DB 379 -----AVEQALRAGQPDVAASLVQNLSSEQLLAEQNIATILRWKMDLPDLSLAST 428
QY 433 MDKYHRRWLVWLAALL-----LAAALFFPL-----LL-----KKD 464
DB 429 PRLIILLYGWAALACQLDAABELAGQLARELPAPDESQAORDLLAQWQALSQVVIARGRD 487
QY 465 RKAARGSRRTALLHSADGAGVERLVGALASALSQMLPRVAV---DLWSRRELSAHGAL- 520
DB 488 IDKAEAHCREAL-----QDLAG-ER-YGTRLOCLSTLS-NLAVTRGDFWQARNYN-RDALE 539
QY 521 -----AWFHRRRILOEGGVV-----ILLF 541
DB 540 FAQRVGNPLFEALVHYDRARVLQARGEVARABEEVRQGLERLQHLPAQRVYAVRGRLILY 599
QY 542 SPAVAQCOQWLQLOTFEPGPHDALAWLS-----CVLPDFLOGRAT 583
DB 600 -----RGYLSLALQP---DEARKWIKOGIETRSCRVDVSLVIGYCVLAS-LEGR-L 646
QY 584 GRYVGVV-----FDGLLHPDSVPSFRVAPLPSLPQ----- 615
DB 647 GNYAAAFARLGDVERLMAWDIPPIYLYLAATILKELWLAQGOQLAGWMLQRLGGTYG 706
QY 616 -----LPAPFDALQGCSTAGRPADRVERTVQALRSALDS 651
DB 707 GQATPPECSPILLPLHVELLQAGLERREGRPPEAAARRLDRLARSTREN 754

RESULT 13
A55148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N;Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55148
R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associated with the rat osteotesticular protein-tyrosine phosphatase
A;Reference number: A55148; MUID:95074080; PMID:7527035
A;Accession: A55148
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1711 <MAU>
A;Cross-references: UNIPARC:UPI000004DC1D; GB:I36884
C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosinase
C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repeat
C;KeyWords: phosphoprotein; phosphoric monoeester hydrolase; receptor; transmembrane prote
F;18/Domain: signal sequence #status predicted <SIG>
F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MAU>
F;1174-1398/Domain: protein-tyrosine-phosphatase homology <FPI>
F;1350/Active site: Cys (phosphotyrosine intermediate) #status predicted
F;1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.8%; Score 102.5; DB 1; Length 1711;
Best Local Similarity 20.8%; Pred. No. 17;
Matches 149; Conservative 79; Mismatches 229; Indels 267; Gaps 40;

QY 43 DGVVCLPLGSLQSA-----PGPVLPVTRLQTEL-VLRCFPQK-----TDC 80
DB 333 DGVVCLSGPMESTSLTGPCECNVAFPGP-LPPGHVTLQLKVLGPDVAVVEGVTWLAES 391

QY 81 ALRRVVVHLAVHGHWAEPBEAGKSDSELOESNRNASLQAQVLSFOAYPIARCALLEVQV 140
Db 392 AALPREVPGARL---WLDGLEASK---QPGREALLYSD-----DAPGSLGNISV 434
QY 141 PADLVQ-----PGQ-----SVGSVAVDPCPEASIGAEVQIWSYTKPRYQKELNLTQOLPD 189
Db 435 PSGATHVIFCGLVFGAHYRVDIASSTGDISQSISG-----YTSPLPPQSLEY----- 481
QY 190 GDNVLLTLDSVEQDFSLYLVRPVDAL---KSLWKYKNTL-----GQNITLNH 236
Db 482 -----ISRSPPDLTTAWGPAPQLEGYKVTWHQDGSQRSBGDLVDLGGPDTLSTL 532
QY 237 TDLVP---CLCIQVW---SLEPDSERVEFCP-----FREDPGAHRNLWH--- 274
Db 533 KSLVPGSSYTVSAWAGNGLGSDSKIHSTRPAPPTNLSLGFAPHAQPAALKASWYHPPGG 592
QY 275 -----IARLRLV---SPGV-----W-QLDAPCCLPKVKTLWCQAPDQSPQPLV 314
Db 593 RDAFHLRLRLPLTLESEKVLPREAQNFSAQLTAGCEVQVQLSTLWGSERS----- 646
QY 315 PPVPQKNATVNEQDFQVAGHPNLCVQVSTWEKVLQACSWADSLGPFKDDMLLVEMKT 374
Db 647 -----SANATGWTP-----PSAPTL-VNVTSDAPTQLQV-SWAHVPQ----- 681
QY 375 GLNNTSVCALEPGSGCTPLPSMASTRAAALGEBLLQDPRSHQCMQLWDDNMGSLWACPM 434
Db 682 GRERYQVTLQESTRTATSTNGP-----KEDGTSFLGLTPGT 718
QY 435 KYTHRRWLVWLACLLIAAA---LFFPLLKKDRKKAARGSTRALLSHSADGAGYERLV- 490
Db 719 KY--KVEVISWAGPLYTAAANSAWYTLIPNE-----LLVSMQAGSAVNVILAW 765
QY 491 -----GALASALS-----OMPLEVAVDLSRRSLSAHGALAWFHRRILQEGGV 536
Db 766 PSGPLOGGACHAQSDAGHLSWQPLKLGQELFMLRLDLPFGHTISMSVRCRAGPLQASTH 825
QY 537 VILLFSPAQAQCOQWLQVTPGP- HDAL-----AAWLS-----CVLPDFLQ 579
Db 826 LVLV-----SVFPGVEDVLCHPEATYALNTWMPAGDVVCLV----- 864
QY 580 GRATGRVY---GVYP-----DGLHPDSVP-SPPRVAPLPSLTQLPAFLDALQGGC 637
Db 865 --VVERLVPGGGTHFVQVNTSGDALLPLNLPMTTSYRLS--LTVLGRNRSWRAVSLVC 920
QY 628 STSA 631
Db 921 STSA 924
RESULT 14
A41185
alpha-2 macroglobulin MUG1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-Apr-1995
C;Accession: A41185
R;Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A;Title: Molecular characterization of the murinoglobulins.
A;Reference number: A41185; MUID:91358495; PMID:1840592
A;Accession: A41185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1476 <OVE>
A;Cross-references: UNIPARC:UPI0000176340; GB:M65736
C;Superfamily: alpha-2-macroglobulin
Query Match 2.8%; Score 101.5; DB 2; Length 1476;
Best Local Similarity 21.4%; Pred. No. 17;
Matches 72; Conservative 44; Mismatches 149; Indels 71; Gaps 16;
QY 86 VVHLAV-----HGHWAEPPEA---GKSDSELOESNRNASLQAQVLSFOAYPIARCALLE 137
Db 137

Db 489 VMAHLSIIQTGNHTHQVEPEAFVKGK-----FALEIPVEFSPVMPMAKMLIYT 536
QY 138 VQVPADLVQPGQSGVSAVDFCPPEASIGAEVQIWSYTKPRYQKELNLTQOLPDGDNVLLTL 197
Db 537 ILDPGEVI--ADSVNFEIEKCLRNKVDLRPST--QSLSPASQTRLOVTAS--POSICGLRAV 592
QY 198 DVSEBQDFGLLYLRPVPDALKSLWKYKNTLGPQNITLNHTDLVP-----CLCIQV 247
Db 593 DQS-----VLLLKPESE--LSPSWIYNLPGMQ-----QNKFPVSSRLSDEQEDCILYSS 639
QY 248 W-----SLEPDSERVEFCPREDPG--AHRNLWHARLVLSPGWQLDAPCC---LPG 296
Db 640 WLAEKHTNLPHGTEKDVYRYVEDMGLTAFNTLMILPLIICFDYGMVPIAPRVBFOLAF 699
QY 297 KVTLCWQAPDQSPQPLVPPVPQKNATVNEQDFQVAGHPNLCVQVSTWEKVLQACSW 356
Db 700 TPBISLSRLTSLKRPBP--PRKDFSSNDPLTETIRKYPPTWV-----WDIVTVNSTGL 753
QY 357 A-----DSLGPFKDDMLLVEMKTLGNNTSVSCALE 385
Db 754 AEVEMTVPTDITETWKAGALCLSNDTGLGLSSVVPVLPQ 789
RESULT 15
A54100
tumor suppressor protein DCC precursor - human
N;Alternate names: colorectal cancer suppressor DCC
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: A54100; A40098
R;Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, B.
Genes Dev. 8, 1174-1183, 1994
A;Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis.
A;Reference number: A54100; MUID:95011532; PMID:7926722
A;Accession: A54100
A;Molecule type: mRNA
A;Residues: 1-1447 <HED>
A;Cross-references: UNIPROT:PA3146; UNIPARC:UPI00000358B3; EMBL:X76132; NID:9453209; PIDN:R;Fearon, E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamilton Science 247, 49-56, 1990
A;Title: Identification of a chromosome 18q gene that is altered in colorectal cancers.
A;Reference number: A40098; MUID:90100559; PMID:2294591
A;Accession: A40098
A;Molecule type: mRNA
A;Residues: 1-750 <FEA>
A;Cross-references: UNIPARC:UPI000016A7D8; GB:M32292; NID:g181492; PIDN:AAA35751.1; PID: C;Genetics:
A;Gene: DCC
A;Cross-references: GDB:119838; OMIM:120470
A;Map position: 18q21.1-18q21.1
C;Keywords: transmembrane protein; tumor suppressor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-1447/Product: tumor suppressor protein DCC #status predicted <MAT>
Query Match 2.8%; Score 100; DB 2; Length 1447;
Best Local Similarity 18.2%; Pred. No. 22;
Matches 125; Conservative 56; Mismatches 183; Indels 322; Gaps 29;
QY 70 LVLRCFQKTCALRV-----RVVHLAVHGHWAEPBEAGKSDSELOESNRNASLQAQVLSF 125
Db 57 VLLDCSAESDRGVPIKWKKGDIHLAL-----GMDERKQSLNSGSLTIQNLHS 105
QY 126 QAYPIARCALLEVQVVPADLVQPGQSGVSAVDFCPPEASIGAEVQIWSYTKPRYQKELNLT 184
Db 106 RHH-----KPDH-----GLYQC-EASLGDGSGSIISRTAKVAVAGPLRFL 143
QY 185 QQLPD-----GDNVLLTLDSVEQDFSLYLVRPVPDALKSLWKYKNTLGPQNITLNHTD- 238
Db 144 SQTESVTAFMGDTVLKCEVGE-----PMPTI---HWQKN---QQDLTPIPGDS 187
QY 239 ---LVPLCLCIQVWSLBPDSERVEFCPFR-----EDPGAHRNLWHI----- 275
Db 188 RVVLPFGALQISRLQPDGDIYRCRSARNPASRTGNEAEVRILSDPGLHRLQYFLQRP 247

Tue Aug 22 11:34:38 2006

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276 ----- 275
Db 248 NVVAIEGDAVLECCVSGYPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNVTTDDSGM 307
Qy 276 -----ARLVLSPGVWQLDAPCCLPGKVTLCWQAPD-QSPCQPLVPPVP- 318
Db 308 YTCVVYKRNENISASAEITVLVP-PWFLNHPNL-----YAYESMDIEFECTVSGKPVPT 361
Qy 319 ---QKNATVNEPQDFQLVAGHENLVCQVSTWEKVQLQACSWADSLGPFKDD---MLIVE 371
Db 362 VNMWKGNDVVPSTYFQIVGGSNLRI-----LGUVKSDEGFYQCVAE 403
Qy 372 MKTGLNNTSVCALEPSGCTP-----LPSMASTRARLGEELLQDFRSHQCMOL 419
Db 404 NEAGNAQTSAQILIVPKPAIPSSSVLPAPRDVVPVLVSSRFVRLS----- 448
Qy 420 WNDNNGSLWACPMCKYIHRRWVLYWLACLLLAALFFELLKKDRRKAAGS-RTALLL 478
Db 449 -----WRPPAE-----AKGNIQTFTVP 465
Qy 479 HSADGAGYERLYGALASALSOMPLR-----VAVDLMSRRELSAHGALAWFHHQ 526
Db 466 FREGDNRERALTTPQGSLOLTGVNLPKPEAMYTFRVVAYNEMGPGESS----- 514
Qy 527 RRRILQEGGVILLFSPAQAQOQWLQ-----LQVTEGPHDALAAWLSCVLPDFLO 579
Db 515 -----QPIKVA-TQPELQVPGPVENLQAVSTSTSLITWEP---PAYAN 555
Qy 580 GR-----ATGRYGVYFDGL 594
Db 556 GPVQGYRLFCTEVSTGKEQNIENV DGL 581
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Search completed: August 16, 2006, 11:46:57
Job time : 48 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:37:41 ; Search time 306 Seconds
(without alignments)
2037.453 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

Sequence: 1 MPVSWFLSLALGRNPFVWS.....SSRPGCCBWDLGPCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	674	1	I17RC MOUSE
2	2281	63.3	791	1	I17RC HUMAN
3	1627	45.1	308	2	Q8BP15 MOUSE
4	838.5	23.3	267	2	Q8N2D7 HUMAN
5	350	9.7	637	2	Q6AZ51 RAT
6	338.5	9.4	637	2	Q8BH06 MOUSE
7	310.5	8.6	617	2	Q8K4C1 MOUSE
8	310	8.6	667	2	Q8NFR9 HUMAN
9	309	8.6	551	2	Q8N8H7 HUMAN
10	307.5	8.5	436	2	Q315F0 MOUSE
11	282.5	7.8	591	2	Q6NSU9 MOUSE
12	280.5	7.8	330	2	Q4RJU4 TETNG
13	214	5.9	311	2	Q8R335 MOUSE
14	206.5	5.7	336	2	Q6ZVW7 HUMAN
15	196	5.4	234	2	Q6PTB8 RAT
16	167	4.6	864	1	I17RA MOUSE
17	166	4.6	234	2	Q8CSD0 MOUSE
18	151.5	4.2	865	1	I17RA HUMAN
19	121	3.4	390	2	Q8N8H8 HUMAN
20	121	3.4	2837	2	Q5ZPA6 DELT
21	120	3.3	638	2	Q3QM15 GAWM
22	117	3.2	482	2	Q8TEC2 HUMAN
23	117	3.2	1217	2	Q2NKJ3 HUMAN
24	116.5	3.2	745	1	I17RD BRARE
25	116.5	3.2	1711	1	PTPRV RAT
26	116	3.2	1388	2	Q57UR7 TRYANOMA
27	115.5	3.2	794	2	Q4SK16 TETNG
28	115.5	3.2	4905	2	Q4FZJ3 LEIMA
29	115	3.2	772	2	Q4Q1V2 LEIMA
30	114.5	3.2	690	2	Q3R490 XYLFA
31	114.5	3.2	690	2	Q3RD47 XYLFA

32	114.5	3.2	1013	2	O53499 MYCTU
33	114.5	3.2	1013	2	Q7T218 MYCBO
34	114.5	3.2	1217	2	Q5RDX3 PONPY
35	114	3.2	767	2	Q3P288 GAWM
36	114	3.2	3168	2	Q881Q4 PSESM
37	113	3.1	427	2	Q7PNN1 ANOGA
38	112.5	3.1	1246	2	Q4KAH7 PSEFS
39	112	3.1	2067	2	Q5DOR2 GIBMO
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41	111	3.1	1181	2	Q4DXU2 TRYCR
42	110.5	3.1	394	2	Q888Z2 PSESM
43	110.5	3.1	698	2	Q87C70 XYLFT
44	110.5	3.1	848	2	Q7WIW4 BORDER
45	110.5	3.1	954	2	Q8VJQ4 MYCTU

ALIGNMENTS

RESULT 1
I17RC MOUSE STANDARD; PRT; 674 AA.
AC Q8K4C2; Q99J43;
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Interleukin-17 receptor C precursor (IL-17 receptor C) (IL-17RC)
DE (Interleukin-17 receptor-like protein) (IL-17RL).
GN Name=il17rc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Gilbert J.M., Gorman D.M.;
RT "Identification of novel IL-17 related receptors.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=129; TISSUE=Mammary tumor;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahy J.J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Rvent=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8K4C2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K4C2-2; Sequence=VSP_014142, VSP_014143, VSP_014144;
CC Note=No experimental confirmation available;
CC -----

O53499 mycobacteri
Q7t218 mycobacteri
Q5rdx3 pongo pygma
Q3p288 shewanella
Q881q4 pseudomonas
Q7pnn1 anopheles g
Q4kah7 pseudomonas
Q5d0r2 gibberella
Q3r999 xyella fas
Q4dxu2 trypanosoma
Q888z2 pseudomonas
Q87c70 xyella fas
Q7wiw4 bordetella
Q8vjg4 mycobacteri

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EMBL; AF458066; AAM77570.1; -; mRNA.
EMBL; BC004759; AAH04759.1; -; mRNA.
Ensembl; ENSMUSG00000030281; Mus musculus.
MGI; MGI:2159336; I117c.

MGI; MGI:2159336; ILL/IC.
Alternative splicing: Glycoprotein: Membrane; Receptor; Signal;
MGI:2159336; ILL/IC.

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SIGNAL		674	Interleukin-17 receptor C.
CHAIN	22		

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TRANSMEM	441	461	Potential.
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CARBØHYD	182		N-linked (GlcNAC. . .) (Potential).

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isoform 2).
/FTID=VSP 014143.

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		MISSING (in isoform 2).
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		R -> C (in Ref. 2).

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CONFLICT 355 S -> L (in rel. 2).
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1 MPVSWFLSLALGRNPVVVSLRIMEPQDTARCSLGLSCHLWDGDVLCPLGSLQSPGV 6

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181 LNLTQQLPDGDNVLLTLDVSEEQDFSLLYLRPVPDALKSLWYKNLTGPQNTLNHTDLV

181 INLTQQLPDGDNVLLTLDVSEEQDFSEFLTYLRKVPFQDAKSLWIKNTLTGPFQNIILNNHLDV
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361 GPFFKODMLLVEMKTNNTSVCALEPSCGTPLPMASTRAARLGEELLQDFRSHQCMQLW

361 GPFFKODMLLVEMKITGLNNTSVCALEPSSGCTPLPFSWASIKRAAKDGEEDDDFFASHQCMQZUR
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541	QY	PSPAAVAQCOOWLOLQTVPEGPHDALAAWMLSCVL	PDFLQGRATGRVGVYFGLLHPDSV	600
541	Db	PSPAAVAQCOOWLOLQTVPEGPHDALAAWMLSCVL	PDFLQGRATGRVGVYFGLLHPDSV	600
601	QY	PSPFRVAPLSLTQLPAPFALDALQGGCST	SAGRPADRVERTVQALRSALDSC	660
601	Db	PSPFRVAPLSLTQLPAPFALDALQGGCST	SAGRPADRVERTVQALRSALDSC	660
661	QY	CCEWDLGPC	TITLE 674	
661	Db	CCEWDLGPC	TITLE 674	

RESULT 2

IL17RC HUMAN	PRT; 791 AA.
ID IL17RC HUMAN STANDARD;	
IAC Q8WVC3; Q6UWD4; Q8NFS1; Q9BR97;	
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.	
DD 01-OCT-2002, sequence version 1.	
DE 07-FEB-2006, entry version 17.	
DE Interleukin-17 receptor C precursor (IL-17 receptor C) (IL-17RC)	
DE (Interleukin-17 receptor-like protein) (IL-17RL) (interleukin-17	
DE receptor homolog) (IL17Rhom).	
DE Name=IL17RC; ORFNames=UNQ6118/PRO20040/PRO38901;	
GN Homo sapiens (Human).	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
(1)	
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).	
RP Gilbert J.M., Gorman D.M.;	
RA "Identification of novel IL-17 related receptors.";	
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	
[2]	
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3). AND VARIANT	

RP SER-182.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell P., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klmowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandusen R.L., Watanabe C., Weiland D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."; *Bioinformatics* 19:2265-2270(2003).
 RT Genome Res. 13:2265-2270(2003).
 PL

GENOME RESEARCH [3] NUCLEOTIDE SEQUENCE [IMAGE SCALE MNNA] (ISOFORM 1).

NCBI/BLAST SEQUENCE ANALYSIS

RP TISSUE=Splice;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsura N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakata S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiwa S., Komai F., Hara R., Takeuchi K., Arima M., Imose N.,

5

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyaama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4), AND VARIANT
RP SER-182.
RC TISSUE=Uterus;
EX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP PROTEIN SEQUENCE OF 21-35.
EX PubMed-15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
[6]
RP ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
EX PubMed-11706037; DOI=10.1074/jbc.M109372200;
RA Haudenschild D., Moseley T., Rose L., Reddi A.H.;
RT "Soluble and transmembrane isoforms of novel interleukin-17 receptor-
RT like protein by RNA splicing and expression in prostate cancer.";
RL J. Biol. Chem. 277:4309-4316(2002).
[7]
RP INDUCTION BY HGF AND VEGF.
EX PubMed-14504135; DOI=10.1038/sj.bj.0705494;
RA Gerritsen M.E., Tomlinson J.E., Zlot C., Ziman M., Hwang S.;
RT "Using gene expression profiling to identify the molecular basis of
RT the synergistic actions of hepatocyte growth factor and vascular
RT endothelial growth factor in human endothelial cells.";
RL Br. J. Pharmacol. 140:595-610(2003).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Soluble isoforms
CC may be produced.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=QBNA3-1; Sequences=Displayed;
CC Note=No experimental confirmation available;

CC Name=2;
CC IsoId=QBNA3-2; Sequences=VSP_014138;
CC Name=3;
CC IsoId=QBNA3-3; Sequences=VSP_014138, VSP_014139;
CC Note=No experimental confirmation available;
CC Name=4;
CC IsoId=QBNA3-4; Sequences=VSP_014138, VSP_014139, VSP_014140,
CC VSP_014141;
CC TISSUE=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed in brain, cartilage, colon, heart,
CC intestine, kidney, liver, lung, muscle, placenta, and prostate.
CC Low expression in thymus and leukocytes. Expressed (at protein
CC level) in prostate and prostate cancer, skeletal muscle, kidney
CC and placenta.
CC -!- INDUCTION: By HGF and VEGF.
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
CC EMBL; AF458065; AAM77569.1; -; mRNA.
CC EMBL; AY358840; AA089199.1; -; mRNA.
CC EMBL; AY359098; AA089456.1; -; mRNA.
CC EMBL; AK029007; BAC04001.1; -; mRNA.
CC EMBL; BC006411; AA06411.1; -; mRNA.
CC EMBL; ENSG00000163702; Homo sapiens.
CC HGNC; HGNC:18358; IL17RC.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Membrane; Polymorphism; Receptor; Signal; Transmembrane.
FT CHAIN 1 20 Interleukin-17 receptor C.
FT SIGNAL 1 20 FTID=PRO_0000011034.
FT TOPO DOM 21 538 Extracellular (Potential).
FT TRANSMEM 539 559 Potential.
FT TOPO DOM 560 791 Cytoplasmic (Potential).
FT CARBOHYD 189 189 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 257 257 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 420 420 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 443 443 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 36 106 Missing (in isoform 2, isoform 3 and
FT isoform 4).
FT FTID=VSP_014138.
FT VARSPLIC 264 278 Missing (in isoform 3 and isoform 4).
FT FTID=VSP_014139.
FT VARSPLIC 579 624 AAARGAALLYSADDSGFERLVGALCALCOLPLRVAVDL
FT WSRR -> GEWEQALGGPPGSOACASSPLSPSVPFSGS
FT GRQGRGSAPLSR (in isoform 4).
FT FTID=VSP_014140.
FT VARSPLIC 625 791 Missing (in isoform 4).
FT FTID=VSP_014141.
FT VARIANT 182 182 L -> S (in dbSNP:708567).
FT CONFLICT 241 241 E -> G (in Ref. 2; AAQ89199).
FT SEQUENCE 791 AA; 86294 MW; E0A636BCB472317 CRC64;
Query Match 63.3%; Score 2281; DB 1; Length 791;
Best Local Similarity 58.9%; Pred. No. 4.5e-170;
Matches 458; Conservative 66; Mismatches 134; Indels 120; Gaps 8;
QY 1 MPVSWFLSLALGRNPVVVSRLMEPQDTARCS----- 34
Db 1 MPVFWLLSLALGRSPVLSRLRVGPQDATHCSVSLPMEPDERLRVQFLAQQLSLA 60
QY 35 -----LGLSCHLWDCGVLC 49
Db 61 PVTATARTALSGLSGADGRREGRGKSWCLSLGGSGNTEPQKKGUSCRWDSDILCL 120
QY 50 PGSLQSAFGPVLVPTRLQTELVLRCPOKTCALRVVVVHLAVHGHWAEPES-----AGKS 105
|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :

Db 121 PGDIVPAGPVLAPTHLQTELVLRCQKTDCLDLRVAHLVHGHWEPEDEKFGGA 180

QY 106 DSELQESRNASLOAQVVLSPQAYPIARCALLEVQVADLVQVQSGVSAVFDFCFEASLCA 165

Db 181 DLGVEPRNASLOAQVVLSPQAYPIARCALLEVQVADLVQVQSGVSAVFDFCFEASLCA 240

QY 166 EQVINSYTKPRYKELNLQQLP-----DGNVLLTLTVSE 201

Db 241 EVRINSYTPRYEKELNHTQQLPDCRGLEWNSIPSCWALPWLNSADGDNVHLVNLVSE 300

QY 202 EQDFSELYLRPVPDALKSWYKNTLGPONITLHNTDLPCLCIQWSLEPDSERVEFCP 261

Db 301 EQHFGLSLYNQVGGPKPRWHKNTLGPQITLHNTDLPCLCIQWLPLEPDSVRNIPCP 360

QY 262 FREDPCGHRNLWHIARLVSPGVWOLDAPCCLPGLKVTLCQWAPDQSPQPLVPPVPPQKN 321

Db 361 FREDPCGHRNLWHIARLVSPGVWOLDAPCCLPGLKVTLCQWAPDQSPQPLVPPVPPQKN 420

QY 322 ATVNEPQDFOLVAGHPNLCVQSTWKEVQLQACSWADSLGFFKDDMLLVEMTKTGLNNTSV 391

Db 421 VTVDKVLFFLLKGGHPNLCVQSTWKEVQLQACSWADSLGFFKDDMLLVEMTKTGLNNTSV 480

QY 382 CALEPSCGCTPLPSMASTRARLGEILLQDFRSHQCHQWLNDDNMGSIWACPMCKYIHRW 441

Db 481 CALEPSCGCTPLPSMASTRARLGEILLQDFRSHQCHQWLNDDNMGSIWACPMCKYIHRW 539

QY 442 VLVWLACLLAALFFPFLLLKDDRRK-----AARGSRRTALLHSDAGGYE 487

Db 540 ALVWLACLLAALFFPFLLLKDDRRK-----AARGSRRTALLHSDAGGYE 598

QY 488 RLVGALASALSQMLRVAVDLWSRRELSSAHLAWFHQRRLIQEGGVILLFSPAIVA 547

Db 599 RLVGALASALSQMLRVAVDLWSRRELSSAHLAWFHQRRLIQEGGVILLFSPAIVA 658

QY 548 QCQWLQIQTVEP---GPHDALAALVSLVLPDFLQGRATGRYGVYDFGLLHPDVSPPF 604

Db 659 LCSEWLQGVSGGAGHGFHDAFRASLSCVLPDFLQGRAPGSYVGCDFRLLHPDVAVPALF 718

QY 605 RVAPFLSLTQLPAFLDALQGCSTAGRAPDRVRYVTOALRSALDSC--TSSEAPG 660

Db 719 RTVPVFLPSQLPFLGNLQOPRPSRGLQERAEQVSRALQPALDSYFHPGPGTAPG 776

RESULT 3

Q8BP15_MOUSE PRELIMINARY; PRT; 308 AA.

AC Q8BP15_MOUSE, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110025H02 product:hypothetical protein, full insert sequence.

GN Name=1117c;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1016/S0076-6879(99)03004-9;

RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."

RL Methods Enzymol. 303:19-44(1999).

RN [2]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC PubMed=16141072; DOI=10.1126/science.1112014;

RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldinis V., Allen J.E., Birney E., Hayashizaki Y.;

Ambei-Impimbato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo C., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasaki Y., Keiso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petkovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sengo S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Tada J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno K., Nakano K., Ninomiya N., Nishio T., Okada M., Ohtsuka C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

RT "The transcriptional landscape of the mammalian genome.";

RL Science 309:1559-1563(2005).

RN [3]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; PubMed=12354683; PubMed=12466851; DOI=10.1038/nature01266;

RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasaki Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).

[5]
RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).

[6]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.145100;
RX MEDLINE=20499374; PubMed=11042159; Sugahara Y., Shibata K., Itoh M.,
RA Carninci P., Shibata Y., Hayateu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).

[7]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).

[8]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaakawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nomazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Tanaka T., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

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CC

DR EMBL; AK075634; BAC35870.1; -; mRNA.

DR Ensembl; ENSMUSG00000030281; Mus musculus.

DR MGI; MGI:2159336; I117c.

KW Hypothetical protein.

SQ SEQUENCE 308 AA; 33799 MW; 16410BDAACAFB66AP CRC64;

Query Match 45.1%; Score 1627; DB 2; Length 308;
Best Local Similarity 99.7%; Pred. No. 3.3e-119;

Matches 307; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 367 MLLVEMKTLGNTSVCALEPSGCTPLPSMASTRARALGEEELLDQFRSHQCMLWDDNNG 426

Db 1 MLLVEMKTLGNTSVCALEPSGCTPLPSMASTRARALGEEELLDQFRSHQCMLWDDNNG 60

QY 427 SLWACPMNDKYHRRWVLTACILAAALPFLILKKDRRAKRSRTALLHLSADGAGY 486

Db 61 SLWACPMNDKYHRRWVLTACILAAALPFLILKKDRRAKRSRTALLHLSADGAGY 120

QY 487 ERLVGLASALSOMPLRVAVDLWSRRELSSAGLAWFHQRRIILQEGGVILLFSPAIV 546

Db 121 ERLVGLASALSOMPLRVAVDLWSRRELSSAGLAWFHQRRIILQEGGVILLFSPAIV 180

QY 547 AQCCQWLQOTVPEPGHDAALAAWLSVLPDFLOGRATGRYGVYFDGLLHSDVSPFRV 606

Db 181 AQCCQWLQOTVPEPGHDAALAAWLSVLPDFLOGRATGRYGVYFDGLLHSDVSPFRV 240

QY 607 APLSLPTLPAPFLDALQGGCSTAGRPADRVETQALRSALDSCSTSSSEAPGCCBWD 666

Db 241 APLSLPTLPAPFLDALQGGCSTAGRPADRVETQALRSALDSCSTSSSEAPGCCBWD 300

QY 667 LGPCTTLE 674

Db 301 LGPCTTLE 308

RESULT 4

Q8N2D7_HUMAN PRELIMINARY; PRT; 267 AA.

AC Q8N2D7;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 21-FEB-2006, entry version 9.

DE CDNA PSEC0233 fig, clone HEMBA1006813.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole embryo;

RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,

RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,

RA Nagahari K., Sugano S., Isogai T.;

RT "HRI human cDNA sequencing project.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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CC

DR EMBL; AK075534; BAC11677.1; -; mRNA.

DR Ensembl; ENSG00000163702; Homo sapiens.

SQ SEQUENCE 267 AA; 29696 MW; 490FICE9699D5B2C CRC64;

Query Match 23.3%; Score 838.5; DB 2; Length 267;

Best Local Similarity 61.4%; Pred. No. 2.6e-57;

Matches 172; Conservative 25; Mismatches 56; Indels 27; Gaps 5;

QY 1 MPVSWFLSLALGNRVVVSRLERLWEPQDTCARCSLGLSCHLWDGVLCLPQSLQAPGPV 60

Db 1 MPVSWFLSLALGNRVVVSRLERLWEPQDTCARCSLGLSCHLWDGVLCLPQSLQAPGPV 60

QY 61 LVPFTELQTLVRCQKTDCLRVVVVHLAVHGHWAEPER-AGKSDSELQSRNAS 116

Db 61 LVPFTELQTLVRCQKTDCLRVVVVHLAVHGHWAEPER-AGKSDSELQSRNAS 120

QY 117 LQAQVWLSFQAYPTIARCALEVQVQPADLVQPQSVGSVAFDCEASLGAEVQIWSYTKPR 176

Qy	239	LVPCLCIQWVSLPDSERVEFCPPEDPGAH--RNLWHIARLRVLSPG-----VQMLDAPCCL	294
Db	198	LLPCMCIEASYLOEDTVRHKKCFRFPWPAFGSDFWKSIKFTDYSQHSQWMAWLTURCPL	257
Qy	295	PGKVTLCQWAPDQSPCOPLVPPVPQKNATVNEPQDFQVAG---HNNLCVQVSTWEKVQL	351
Db	258	KLEASLCWRQDPVTPCKIL-----PNATAKESEGVIYLVNVDLHPQLCFKFS--FENSSH	310
Qy	352	QAC-----SWADSLGPFKDDMLLVEMKTLGNNTSVSCALE-----PSGCTPLPSMAS	397
Db	311	VECPHQSGSLPFSMTVSMDT-QAQQILIHFTSTRTYATFSAWNSPGLGLDSDMPVVSISQ	369
Qy	398	TR-AARLGEELLQDF-RSHQCMQLWNNDDNMGSLW---ACPMQKVIHRRWVWVLAQLILA	452
Db	370	TQGSVPVTLNLIIPFLRQSGCILVWRSQ-VQFAWKHLCP--DVSHRHGLGLLIALGLT	426
Qy	453	AALFFFLKVKDRKAARG-SRTALLIHSADGAGYERLVGALASALSQM---PLRVAVDL	508
Db	427	TLLGLVWLVLCRRLLPGGRTPRVLLHHAADSEARQLVGLAALLTALGGGRDVLVDL	486
Qy	509	WSRRELSAHGALAWPFHORRILQEGGVVILLFSPAAVAAQQQWLQIQTVPEGPHDALAA	568
Db	487	WEGTHVARIGELPWLWAARERVAEREQGVTLMLWSCAGFS-----TACSGDPQTASLR	538
Qy	569	WLSCVLPDPLQGRATGRVGVYFQGLLHPDSVPSFPRVAPLPSLTOLPAFLDALQGGCS	628
Db	539	TLSCAAPRQL-----LLAYFSRLCAKGDIPGFLRALPRYLRDLPRLLRALD----	586
Qy	629	TSAGRPADRVVER-----VTQALRGALDSC	652
Db	587	---ARPATLATSWSHLGAKECLKSELELC	612
RESULT 6			
ID	Q8BH06	MOUSE	
AC	Q8BH06	PRELIMINARY; PRT; 637 AA.	
DT	01-MAR-2003	integrated into UniProtKB/TrEMBL.	
DT	07-FEB-2006	entry version 1.	
DE	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B2030366O11 product:hypothetical protein, full insert sequence (4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430320H14 product:EST AA589509, full insert sequence)		
DE	(3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630048E03 product:interleukin 17 receptor E, full insert sequence) (interleukin 17 receptor E isoform 1).		
GN	Name=Il17re;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;		
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Methods Enzymol. 303:19-44(1999).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;		
RX	PubMed=16141072; DOI=10.1126/science.1112014;		
RA	Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,		
RA	Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,		
RA	Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,		
RA	Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,		
RA	Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,		
RA	Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,		
RA	Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,		
RA	Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,		
RA	di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,		

Db	121	LOAQVLSQAYPTARCVLLEVQVFAALVQFGSGVSVYDCEAFALGEVWINSYTOPR	180			
Qy	177	YKELNLTQOLP-----DGDNVLVLDYSEQDFSLYLRLPVPDALKSLWKNT	227			
Db	181	YEKLNHTQOLPALPWLNVSAUGDNVHLVNVSEEHQFGLSLYVWQVQPPKPRWHKNLV	240			
Qy	228	GPONITL-NHTDLVPLCLTQVWSLEPDSERVEFCPPREDP	266			
Db	241	RPPPSQVHSHCRMPV-----QRTQ-CHIREDP	267			
RESULT 5						
ID	Q6AZ51	RAT				
AC	Q6AZ51	PRELIMINARY; PRT; 637 AA.				
DT	13-SEP-2004	integrated into UniProtKB/TrEMBL.				
DT	13-SEP-2004	sequence version 1.				
DT	07-FEB-2006	entry version 1.				
DE	Similar to Interleukin 17 receptor E isoform 1.					
GN	Name=Il17re;					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;					
OC	Muridea; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Lung;					
RX	MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk R.A.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,					
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences."					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Lung;					
RA	Director MGC Project;					
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.					
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms					
CC	Distributed under the Creative Commons Attribution-NonDerivs License					
CC	-----					
DR	EMBL; BC078742; AAH78742.1; -; mRNA.					
DR	Ensembl; ENSRNOG00000009204; Rattus norvegicus.					
DR	GO; GO:0004872; F:receptor activity; IEA.					
KW	Receptor.					
SQ	SEQUENCE 637 AA; 70852 MW; BB6C71838AB1C9D5 CRC64;					
Query Match 9.7%; Score 350; DB 2; Length 637;						
Best Local Similarity 27.9%; Pred. No. 2e-18;						
Matches 142; Conservative 57; Mismatches 216; Indels 94; Gaps 21;						
Qy	204	DFGFLY-----LRVPDALKSLWY-----	238			
Db	138	EFSGDLLPEVQAVRVTIPPGFEANRVLCTQVWALECEDMSFPDTQIVSGHTVDLPYEF	197			

Qy	239	LVPCLCTQVWSLEPDSERVEFCPPREDPAH-RNLWHIARLVLSPG----	294
Db	198	LLPCMCIEASYLQSDTVRHKKCPFRSPWEAYGSDFWKSIIFTDYSQHSQWMAITLRCPL	257
Qy	295	PGKVTLCQWAPDQSPCPPLVPPVQKNATVNEPODFOLVAG---HPNLCVQVSTWEKVL	351
Db	258	KLEASLCLWRQDPVTPCKIL-----PNATAKESGWIENVDLHPOLCPKFS-FENSSH	310
Qy	352	QAC-----SWADSLGPFKDDMLLVEMTKTGLNNTSVCALE-----	397
Db	311	VECPHQSGLSPSWTVMST-QAQLILHFSTRYATFSAWNSPGLGLDSDNTFYISIQ	369
Qy	398	TR-AARLGEELLQDF-RSHQWQWLNDDNMGSLW---ACPMCKYIHRRWLVWLAALLA	452
Db	370	TQGSVEVTNLIIIFLROGSCILVWRS-VQFANKHLLCP--DVSHRLGLLILALLGLT	426
Qy	453	AALFFILLKDRRKAARG-SRTALLHSADGAGVERLVGALASALSM---PLFVADL	508
Db	427	TLLGVVIVLFCRLLPGGRTPLVLLHAADSEAQRRLVGALAEELLRTALGGGRDVI	486
Qy	509	WSRRLSAHGALAWFHORRILQEGSVILLFSPAAVAQCOQWLQTVPEPGPHDLAA	568
Db	487	WEGTHVARTIGPLPWLWAARERVARQGTVLLWSGAFS-----TACSGDPQTASIR	538
Qy	569	WLSCLVLPDFLOGRATGRVGVVFDGLLHPDSVPSPFRVAPLSFTQLPAPFDALOGGS	628
Db	539	TLSCAAPROL-----LLAYFSRLCAKGDIFGPLRALPRYRLRLDLPLRLALD----	586
Qy	629	TSAGRAPDRVER-----VTQALRSALDSC	652
Db	587	---ARPATLTSWSHLGAKECLKSLRLC	612
RESULT 6			
ID	Q8BH06	MOUSE	
AC	Q8BH06	PRELIMINARY; PRT; 637 AA.	
DT	01-MAR-2003	integrated into UniProtKB/TrEMBL.	
DT	01-MAR-2003	sequence version 1.	
DT	07-FEB-2006	entry version 20.	
DE	Adult male corpora quadrigena cDNA, RIKEN full-length enriched		
DE	library, clone:B230366011 product:hypothetical protein, full insert		
DE	sequence (4 days neonate male adipose cDNA, RIKEN full-length enriched		
DE	library, clone:B430320H14 product:EST AAS89509, full insert sequence)		
DE	(3 days neonate thymus cDNA, RIKEN full-length enriched library,		
DE	clone:A630048E03 product:interleukin 17 receptor E, full insert		
DE	sequence) (interleukin 17 receptor E isoform 1).		
GN	Name=Il17re; (Mouse).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigena, and Thymus;		
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Methods Enzymol. 303:19-44(1999).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigena, and Thymus;		
RX	PubMed=16141072; DOI=10.1126/science.1112014;		
RA	Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,		
RA	Oyama R., Ravasi T., Lenhard B., Wells C., Kodzi R., Shimokawa K.,		
RA	Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,		
RA	Davis M.J., Wilm M., Lenhard B., Allen J.E.,		
RA	Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,		
RA	Bansal K.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,		
RA	Chiu K.P., Chowdhury V., Christoffels A., Clutterbuck D.R.,		
RA	Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,		
RA	di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,		

RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingers T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwana A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motaguchi-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori P., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RT "The transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563 (2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG Riken Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome",
RL Science 309:1564-1566 (2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozaki-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kaga I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs",
RL Nature 428:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=20185660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection",
RL Nature 409:685-690 (2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes",
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer",
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, and Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kaga I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Inamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RA Li T., Li X., Liu L., Chang Z., Fu X.-Y.,

Tue Aug 22 11:34:38 2006

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RESULT 10
Q315F0_MOUSE PRELIMINARY; PRT; 436 AA.
ID Q315F0_MOUSE
AC Q315F0;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin 17 receptor E isoform 5 (Interleukin 17 receptor E isoform
GN 4).
DN Name=Il17re;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
CC [1]
RN NUCLEOTIDE SEQUENCE.
RP Li T., Li X., Liu L., Chang Z., Fu X.-Y.;
RT "Identification and Functional Characterization of A Novel Interleukin
RT 17 Receptor: A Possible Mitogenic Activation Through RAS/Mitogen-
RT Activated Protein Kinase Signaling Pathway.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; DQ92341; AA285960.1; -; mRNA.
CC EMBL; DQ92340; AA285959.1; -; mRNA.
CC GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 436 AA; 48574 MW; CAB5DA43BF6D2F56 CRC64;
Query Match 8.5%; Score 307.5; DB 2; Length 436;
Best Local Similarity 27.4%; Pred. No. 2.7e-15;
Matches 125; Conservative 51; Mismatches 214; Indels 67; Gaps 18;
Qy 243 LCIQWLSLEPDSERVFECFFEDPGAH-RNIWHIARLRLVSPG---VWQLDAPCCLPGKV 298
Db 1 MCIEASYLQEDTVRRKKCFQSPPEAYSGDFWQSGIRFTDYSQHNQMVNALTRLCPFLKEA 60
Qy 299 TLQWQAPDQSCQPLVPVPVKNAVTNPPQDFQLVAG--HPNLQVOVSTWEKVQLQAC- 354
Db 61 SLCWRQDPLTPCETL-----PNATAQSEGWYILENVDLHPQLCFKS-FENSSHVECP 113
Qy 355 -----SWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCG---TPLPSMASTRARLIG 404
Db 114 HQSGSLPSTWTSMDT-QAQLTLHPFSRTYATFSAASDPGLGPDTPMPVYISIQTQGS 172
Qy 405 EELLQD-----FRSHQCHQLWNDNWSGLW---ACPMDKYTHRRVWLVWLACLLAAALF 456
Db 173 VPVTLDLIIPFLRQENCLVWRSD-VHFAWKVLCP--DVSHRHGLLILALLATLALV 229
Qy 457 PFLILKKDRRKAARG-SRTALLHSGADGAGYERLVGALASALSQM---PLRVAVDLWGRR 512
Db 230 VVVLVLLGRLLPGSGRTPVLLHAAADSEAQRRLVGALAEILLRTALGGGRDIVDLWEGT 289
Qy 513 ELSAHGALAWFHQRRRILOEGGVILLPSPAQAQCQWLOIQIVPEGPHDALAAWLSC 572
Db 290 HVARIGPLFWLAARERVAREQGTVLLWNCAGPS-----TACSGDPQAASRLTLIC 341
Qy 573 VLPDFLQGRATGRYGVGVDFGLLHPDPSVPSPRVPAPLFLPTQLPAFLDALQGGCSTA- 631
Db 342 AAPREL-----LLAYPSRLCAKGDIDPRLALPRYVLLRDLPRLLFALDAQPATLAS 393
Qy 632 -----GRPADRVERTQA-----LRGALDSCTSSESSEAP 659
Db 394 SWSHLGAKRCLKNRLEQCHLLEAAKDDYQGSTNSP 430
RESULT 11
Q6NSU9_MOUSE PRELIMINARY; PRT; 591 AA.
ID Q6NSU9_MOUSE
AC Q6NSU9;

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Db 430 LGGGRDVIDLWEGTHVARIGPLWMAARVAREOQTVLLWNCAGPS-----TA 481
Qy 558 VERPGHDAALWLCVLPDFLQGRATGRYGVYFGLLHPDSVSPFRVAPLFLSLPTQLP 617
Db 482 CSGDQPAASRLTLCAAPRL-----LLAYFSLCAKGDIPRLALPRYLLRLDLP 533
Qy 618 AFLDALOGGCSFSA-----GRPADRVERVTOA-----LRSALDSCTSSEAP 659
Db 534 RLLRALDAQPATLASSWSHLGAKCLKNRLEQCHLLELEAAKDYQGSTNSP 585

RESULT 12
Q4RJU4 TETNG
ID Q4RJU4 TETNG PRELIMINARY; PRT; 330 AA.
AC Q4RJU4;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome 9 SCAP15033, whole genome shotgun sequence.
GN ORFNames=GSTENG00033274001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN RP NUCLEOTIDE SEQUENCE.
RC PubMed=15496914; DOI=10.1038/nature03025;
RA Jallou O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jarre D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Basila C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Creaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin V., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN RP NUCLEOTIDE SEQUENCE.
RC Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL; CAAB01015033; CAG11338.1; -; Genomic DNA.
SQ SEQUENCE 330 AA; 36170 MW; 1D189B0B715289D2 CRC64;

Query Match 7.8%; Score 280.5; DB 2; Length 330;
Best Local Similarity 29.8%; Pred. No. 2.4e-13;
Matches 89; Conservative 36; Mismatches 103; Indels 71; Gaps 12;

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Db 19 CP----PASSRW--RWSLLFTGVLLFSLFFLGAYFIQALGYMWRWLEKDDLKGVGGS 73
Qy 474 TALLHSADG-AGYERLVGALASALSQMLPRVAVDLMSRRLSAGHALWPHHQRRLQ 532
Db 74 QAVLLYPPDGPALPKLNRGLSSILRTGLFTVSLDLSQGLSALGPPVPLHSLNQVR 133
Qy 533 EGGVILLFSPAQAQCOQW-----LQ-----LQTPGPHDALAALWLCVLP 577
Db 134 HGGKVLLVLTQATWLRAEENGAQSWERKVASLEKNKVMDTVSPASSDFTASLSCVLADH 193

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Qy 578 LQGRATGRYGVYFGLLHPDSVSPFRVAP-----LFSLPQLPAFLDALOGG---C 627
Db 194 LQGRAGERFMLEVQPSL--PPKPGGFRPLPGLFGLHYVLSQSLGELTLAGAGPVS 251
Qy 628 STSACRPADRVERTVQA-----LRSALDSCTSSEAPGCCSEWDLGP 669
Db 252 NASARRRRAGVLRMASRFLARGLSGSLTGTLLHIRTTSQCMGD---GVEDSWETMP 306

RESULT 13
Q8R335 MOUSE
ID Q8R335 MOUSE PRELIMINARY; PRT; 311 AA.
AC Q8R335;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE I117re protein.
GN Name=I117re;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.; STRAIN=C2ECH II;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2ECH II; TISSUE=Mammary tumor metastasized to lung.
RC MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; BC026737; AAH26737.1; -; mRNA.
DR Ensembl; ENSMUSG00000043088; Mus musculus.
DR MGI; MGI:1889371; I117re.
SQ SEQUENCE 311 AA; 34103 MW; 00E706D6617CFF15 CRC64;

Query Match 5.9%; Score 214; DB 2; Length 311;
Best Local Similarity 27.0%; Pred. No. 3.8e-08;
Matches 89; Conservative 32; Mismatches 141; Indels 68; Gaps 12;

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Db 21 SAAMSDPLGP-----DTMPPPVVISQTQGVVPVMDL 54
Qy 411 ----FRSHQCQQLWDDNDNGSLW---ACPMDKYIHRRWVLMVLAALLAALFFFLILKK 463

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QY      464 DRKKAARG-SRTALLHSADGAGYERLVGALASALSQM---PLRVAVDLSRRELSAHGA 519
Db      112 RRLPGSGRTRPVLLHHAADSEARQLVGALELLRTALGGGRDVTVDLWEGTHVARIGP 171
QY      520 LAWFHQHRRILQEGGVVILFSPAAVQCCQWLQQTVEPGPHDALAAWLSCVLPDFLQ 579
Db      172 LPLWLAARERVAREQGVVLLLMNACGFS-----TACSGDQQAASLRTLLCAARPL- 222
QY      580 GRATGRYGVYFDGLHPSVSPFRRVAPLSLPTQLPAFLDALQGGCSTSA-----GR 633
Db      223 -----LLAYFSLCAKGDIPRLRALPRYLLRDLPRLLRALDAQPATLASSWSHLGA 275
QY      634 PADRVERTQA-----LRSLDSCITSSEAP 659
Db      276 KRCLKNRLEQCHLLEAAXDYQGSTNSP 305

RESULT 14
Q6ZVW7_HUMAN PRELIMINARY; PRT; 336 AA.
ID Q6ZVW7_HUMAN AC Q6ZVW7
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 8.
DE CDNA FLJ1993 fis, clone SPLEN2017104.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Magatsuma M., Murakawa K., Kaneshori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK123987; BAC85743.1; -; mRNA.
DR Ensembl; ENSG00000188263; Homo sapiens.
SQ SEQUENCE 336 AA; 37651 MW; 467B45E0320554BD CRC64;

Query Match 5.7%; Score 206.5; DB 2; Length 336;
Best Local Similarity 23.8%; Pred. No. 1.6e-07;
Matches 86; Conservative 53; Mismatches 148; Indels 75; Gaps 16;

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Db 9 LTSSTAMQCVSDGCAMLLVRASITLHERLGLLEACAMS-LDTQET----- 54
QY 126 QAYPIARCALLEVQVPADLVQPGQSGVAGFDCPEASIGAEVQIWSYTKPRY-----OK 179
Db 55 -----QCQSVWVARASHRQQRGRL-QVHFGCFVSAQHLVTLRTIPHFCGVQLDQR 107
QY 180 ELNLTQQLP---DGDNVLLTLDV-----SEQDQSFLLYLRL-----PVPDAKSLMWX 224
Db 108 HLVEAGKLSYWDNRRLKALLVQVPRASGSPDYLYLCLKRFCEADAGAPVRVANSV--- 164
QY 225 NLTGQNTLNHTDLVPLCLIQVWSLEPDSERVFPCPFREDPGAHRNLWHIARLVLSFG 284
Db 165 ----PQAVFLPYSQBLPCLCLEGWSATPDVAIRIQICPFENDTEALEVLMDTVYHPESQT 220

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Db      221 LSWE---PACPVSQVHSLCWRPFGAGCRKL-----QQSQLVHRVQVYPLVDTQPQCLK 273
QY      343 VSTWEKVLQACSWADSLG-PFKDDMLLVEMKTLGLNNTSVCALEPSCG-TPLPFSMASTRA 400
Db      274 FST-----SWGSWRCPPF-----QRRFPPTPTSCCTCVTCGSHSLPANASRP 318
QY      401 AR 402
Db      319 AR 320

RESULT 15
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ID Q6P7B8_RAT AC Q6P7B8
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 12.
DE LOC362417 protein (Fragment).
DE Name=LOC362417;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
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RC TISSUE=Prostate;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McWeary P.J., McKernan K.J., Abramson R.D., Mullahy S.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC061739; AAHG1739.1; -; mRNA.
DR RGD; 735148; I117re.
FT NON TER 1
SQ SEQUENCE 234 AA; 25458 MW; 250BB45C58CBDE63 CRC64;

Query Match 5.4%; Score 196; DB 2; Length 234;
Best Local Similarity 31.6%; Pred. No. 6.8e-07;
Matches 73; Conservative 17; Mismatches 107; Indels 34; Gaps 7;

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Db 4 CP--DVSHRHGLGLLILALLGLTLLGVVLVLCRLLPGGRTRPVLLHHAADSEARQL 61

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Qy	607	APLPS	LP	TLQ	PAFLDAL	QCGCST	SAGRPAD	RVER-----	VTOALRSAL	DSC	652
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Search completed: August 16, 2006, 11:46:08
Job time : 311 secs

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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:46:22 ; Search time 52 Seconds
(without alignments)
1134.532 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSFLLSLALGRNPVVVS.....SSEAPGCCSEWDLGPCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCFUS_COMB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2339	64.9	705	2	US-09-747-259-14
2	2339	64.9	705	2	US-09-816-744-14
3	2281	63.3	791	2	US-10-104-047-3296
4	310.5	8.6	617	2	US-09-188-930-303
5	310.5	8.6	617	2	US-09-312-283C-303
6	310	8.6	667	2	US-09-747-259-16
7	310	8.6	667	2	US-09-816-744-16
8	193.5	5.4	226	2	US-09-893-737-328
9	167	4.6	864	1	US-08-620-694A-2
10	167	4.6	864	2	US-09-022-255-2
11	167	4.6	864	2	US-09-022-696-2
12	167	4.6	864	2	US-08-978-773-2
13	167	4.6	864	2	US-09-022-253-2
14	167	4.6	864	2	US-09-022-260-2
15	167	4.6	864	2	US-09-022-259-2
16	167	4.6	864	2	US-09-022-257-2
17	167	4.6	864	2	US-09-549-679-2
18	167	4.6	864	3	US-08-488-728-2
19	151.5	4.2	866	1	US-08-620-694A-10
20	151.5	4.2	866	2	US-09-022-255-10
21	151.5	4.2	866	2	US-09-022-696-10
22	151.5	4.2	866	2	US-08-978-773-4
23	151.5	4.2	866	2	US-09-022-253-10
24	151.5	4.2	866	2	US-09-022-260-10
25	151.5	4.2	866	2	US-09-022-259-10
26	151.5	4.2	866	2	US-09-022-257-10

Sequence 10, Appl
Sequence 1, Appl
Sequence 403, App
Sequence 4, Appl
Sequence 412, App
Sequence 125, App
Sequence 2263, App
Sequence 214, App
Sequence 2, Appl
Sequence 8253, Ap
Sequence 2, Appl
Sequence 18, Appl
Sequence 6842, A
Sequence 10063, A
Sequence 10064, A
Sequence 20327, A
Sequence 28, Appl
Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-747-259-14
; Sequence 14, Application US/09747259
; Patent No. 6569645

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: VanLookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381C1P1(US)
CURRENT APPLICATION NUMBER: US/09/747,259

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/311,832

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: US 60/172,096

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/US99/31274

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: US 60/175,481

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/US00/04341

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 60/191,007

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/07532

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/15264

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: US 60/213,087

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: US 09/644,848

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: PCT/US00/23328

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-14

Query Match      64.9%; Score 2339; DB 2; Length 705;
Best Local Similarity 66.3%; Pred. No. 1.4e-244;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPDQTARCSLGLSCHLWDGVDVLCPLGSLQSPGPV 60
DB 1 MPVSWFLSLALGRSPVLSLRLVGPQDATHCSPLSCLRLWSDILCLPGDIVPAPGPV 60

QY 61 LPVTRLOTELRLRCQKTDCLARVVRVVHLAVHGWABPEE----AGKSDSELQSRNAS 116
DB 61 LAPTHLOTELRLRCQKTDCLCLRVAVHLAVHGWABPEEDEEKEFGGAADSGVEPRNAS 120

QY 117 LOAQVVLFOAYPIARCALLEVQVPADLVQPCQSVGSVAVDFCFEASLGAEOIWSYTKPR 176
DB 121 LOAQVVLFOAYPIARCALLEVQVPADLVQPCQSVGSVAVDFCFEASLGAEOIWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEDQSFLLYLRLPVPDALKSLWYKNLT 227
DB 181 YQKELNHTQQLPALPWLNVSGADGNVHLVNLVSEEQHFGLSLYWNVQVQPPKPRMHKNLT 240

QY 228 GPQNTITLNTDLVPCLCIQVNSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSPGVWQ 287
DB 241 GPQIITLNTDLVPCLCIQVNPDPDSVTRNITCPREDPRAHQNLWQAARLLTLQSWL 300

QY 288 LDAPCCLPGKVTLCQAPDQSPCQPLVPPVPOKNAVNEPQDFQLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPAEALCWAPGDPCCQPLVPLSWENVTVDKLVLEFPLKHPNLCVQVNSSE 360

QY 348 KVQLQACSWADSLGPFKDDMLIVEMKTLGNNTSVCALEPSGCTPLPSMASTRARLGEEL 407
DB 361 KLQLOECLWADSLGPLKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

QY 408 LODFRSHOCMQLWNNDDNGSLWACPMCKYIHRRWLVWLACLLLAALFFFLILKKDRRK 467
DB 421 LODLQSGQCQLW--DDDLGALWACPMCKYIHKRWLVWLACLLFAALSLILLLKKDHAK 479

QY 468 -----AARGSRRTALLHSADGAGYERLVGALASALQMPLRVAVDLWSRRE 513
DB 480 GWRLLLKQDVRSAAAARG-RAALLYSADDSGFELVGLASALCQLPLRVAVDLWSRRE 538

QY 514 LSAHGALAFHFFHQRRILOEGGVWILLFSPAFAVQCOQWLQOTVEP---GPHDALAAWL 570
DB 539 LSAQGPVAFWFAHQRRTLOEGGVVLLFSPGVALCSEWLQDGVSGPGAHGPHDAFRASL 598

QY 571 SCVLDPDFLOGRATGRYGVYFGILLHPDSVPFRVAPLFSITPOLPAFLDALQGCSTSS 630
DB 599 SCVLDPDFLOGRAPGSYGVGACFDRLLHPDAVPALFTVFTPLPSQLDFLQALQOQPRAPR 658

QY 631 AGRPADRVERVTQALRSALDSC--TSSSEAPG 660
DB 659 SGRLQERAEQVSEALQPALDSYFHPGTPAG 690

RESULT 2
US-09-816-744-14
; Sequence 14, Application US/09816744
; Patent No. 6579520
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Qy 571 SCVLPDFLOGRATGRYGVYFDGLLHPSDVSFSPFRVAPLFSLTQLPAFLDALQGGCSTS 630
Db 599 SCVLPDFLOGRATGRYGVYFDGLLHPSDVSFSPFRVAPLFSLTQLPAFLDALQGGCSTS 658
Qy 631 AGRPADRVERVTOALRSALDSC--TSSEAPG 660
Db 659 SGRLOERAEQVSRALQPALDSYFHPGTPAPG 690

RESULT 3
US-10-104-047-3296
; Sequence 3296, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cdna
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3296
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3296

Query Match 63.3%; Score 2281; DB 2; Length 791;
Best Local Similarity 58.9%; Pred. No. 3.4e-238;
Matches 458; Conservative 66; Mismatches 134; Indels 120; Gaps 8;

Qy 1 MPVSWLLSLALGCRNPVWLSLELMEPQDARCS----- 34
Db 1 MPVFWLLSLALGRSPVWLSLERLVGPQDATHCSVPSLEPMDERLRVQFLAQSLSLA 60
Qy 35 -----LGLSCHLWDGVLCL 49
Db 61 PVTAAARTALSGLGDGRRRGRGKSWVCLSLGSGNTEPQKGLSCLRLWDSILCL 120
Qy 50 PGSLOASRGVLPVPTLQTLVLRCPQKTDCLALRVVVHVLVHGWAEPE-----AGKS 105
Db 121 PGDIVPAPGVLAPTHLQTLVLRCKETDCDLCLAVHVLVHGWAEPEDEBEKFGAA 180
Qy 106 DSELOQRNASLQAQVVLSPQAYPIARCALLEVQVADLVQPCQSGVSAVPCDFEASLGA 165
Db 181 DLGVEEPRNASLQAQVVLSPQAYPTARCVLLEVQVPAALVQFCQSGVSVYDCFEAALGS 240
Qy 166 EVOIWSYTKPRYOKELNLTQOLP-----DGNVLLTLDVSR 201
Db 241 EVRIMSYTPRYEKELNHTQOLPDCRGLEVMNSIPSCWALPWLNVSGADGNVHLNVSE 300
Qy 202 EQDFSLLYLRVPVDPALKSILWYKNLTPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCP 261
Db 301 EQHFGLSLYWNQVQGPPEKRWKHLNLTGPIIILNHTDLVPCLCIQVWLEPDSVRNICP 360
Qy 262 FREDPGARNLWHIARLVSPGWQIDAPCCLPVPGKVTLCWQAPDQSPQPLVPPVQPN 321
Db 361 FREDPPRAHNLWQARLRLTLQSWLLDAPCSLPAAALCWAPAGDPCQPLVPPLSWEN 420
Qy 322 ATVNEPQDQFVAGHNLVQVSWTEKVOIACSWADSLGPPFKDDMLLVEMKTLGNTSV 381
Db 421 VTVDKVLPEPLLGHENLVCQVNSSEKIQECLWADSLGFLKDDVLLLETGTPQDNRL 480
Qy 382 CALEPSGCTPLPMSASTRAARLGEELLQDPRSHQCMQMLNNDNMGLMACPMKYIHRW 441
Db 481 CALEPSGCTSLPASKASTRAARLGEYLLQDLSQCCQLQW-DDDLGALMACPMKYIHKRW 539
Qy 442 VLWVLAALLAAALFFFLKDKORR-----AARGSTALLHSDAGAGYE 487
Db 540 ALWVLAALLFAAALSILILLKODHAGWLRLKQDVRSAGAAARG-RAAALLYSADDSGFE 598

Qy 488 RLVGALASALSQMLRVAVDLWSRRBELSAHGALEWHFHHRRRILOBGGVVILLFSPAAVA 547
Db 599 RLVGALASALCQLPLRVAVDLWSRRBELSAQGPVAMFHAQRQTLOEGGVVLLFSPGAVA 658
Qy 548 QCOQWLOLQTVBP---GPHDALAAWLSCVLPDFLOGRATGRYGVYFDGLLHPSDVSFSP 604
Db 659 LCSEWLQDQVSGFGAHPHDAFRASLSCVLPDFLOGRATGRYGVYFDGLLHPSDVSFSP 718
Qy 605 RVAPLFSLTQLPAFLDALQGGCSTSAGRPADRVERVTOALRSALDSC--TSSEAPG 660
Db 719 RTVVFVTLFSQLPDLFALQOQPRAPSRGRLOERAEQVSRALQPALDSYFHPGTPAPG 776

RESULT 4
US-09-188-930-303
; Sequence 303, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011cl
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-303

Query Match 8.6%; Score 310.5; DB 2; Length 617;
Best Local Similarity 25.7%; Pred. No. 4.6e-24;
Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;

Qy 224 KNLGTQNTILNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAH-RNWHIARLVLS 282
Db 183 KIVSGGHTVDLPYEFLLPQMCIEASYLQEDTVRRKKCPQSWPEAYGSDFWQSIPTDYS 242
Qy 283 PG---VWQLDAPCLPGKVTLCWQAPDQSPQPLVPPVQKNATVNEPQDFQLVAG---H 336
Db 243 QHNQWYMATLRCPLKLEASLCWRQDPLTPCETL-----PNATAQSESEGYILENDLH 296
Qy 337 PNLGVQVSWTEKVQLQAC-----SWADSLGPPFKDDMLLVEMKTLGNTSVCALEPSG 388
Db 297 PQLCPKES-FENSSHVECPHQSGSLPSWTVMST-DAQQLTLHFSSTYATFSAAMSDPG 354
Qy 389 C---TLPMSASTRAARLGEELLQD-----FRSHQCMQMLNNDNMGLMACPMKYIHR 440
Db 355 LGPDTMPVPVYSIQSGSVPTDLDLIIPFRQENCILVRSQ-----VHFA 401
Qy 441 WVLV-----WLACILLAAALFFFLKDKORRKAARGSTALLHSDAGAGYERLVGAL 493
Db 402 WKHVLCPDAPYPTQLL-----RSLGSGRTFVPLLHHAADSEBAQRRLVGL 448
Qy 494 ASALSQW---PLRVAVDLWSRRBELSAHGALEWHFHHRRRILOBGGVVILLFSPAQAQ 550
Db 449 AELLRTALCGGRDVIVDLWEGTHVARIGPLPWLWAARERVARQGTIVLLWNCAGPS--- 505
Qy 551 QMLQLQTVBPGHDAALAAWLSCVLPDFLOGRATGRYGVYFDGLLHPSDVSFSPFRVAPL 610
Db 506 ----TACSGDPQAAASLRLLCAAPRL-----LLAYFSRLCAKGDIPRLRALPRY 552
Qy 611 SLPTQLPAFLDALQGGCSTS-----GRPADRVERVTOA-----LRSDLDSCSTSSSEAP 659
Db 553 RLRLDLFRLRLDALDAQPATIASWSHLGAKRCLKNRLEQCHLLEBAKDDYQGSTNSP 611

us-10-719-202-2.ra1

Tue Aug 22 11:34:37 2006

```

; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-747-259-16

Query Match      8.6%; Score 310; DB 2; Length 667;
Best Local Similarity 28.1%; Pred. No. 5.9e-24; Indels 62; Gaps 18;
Matches 130; Conservative 56; Mismatches 214;

QY 224 KNLGTQNTLTNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAH-RNLW---HTARLR 279
DB 223 KIVSGGHTVELPYEFLLPCLCIEASYLOEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 282
QY 280 VLSPGVWQLDAPCCPLPGKVTLCWQAPDQSPQBLVPPVPQKNTVNEPQDF---QLVAGH 336
DB 283 QHTQVMWALTLCPLKLEAALCORHDWHTLCKDL-----PNATARESOGWYVLEKVDLH 336
QY 337 PNLGVQVSTWEKVQLQA-----CSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSPGC 389
DB 337 PQLCFKPFSGNSHVECPHOTGSLTSWNVSMDT-QAQLLILHFSRRHATFSAWSLPG 395
QY 390 ---TPLPSMASTRARLGEELLQD-----FRSHQCMQLNDDNMGSLW---ACPMKYIH 438
DB 396 GQDTLVPPVTVTSQARGSSPVSLDLIIPFLRPGCCVLVWRSD-VQFAWGLLCPDVSYRH 454

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.101LC2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mouse
; US-09-312-283C-303

Query Match      8.6%; Score 310.5; DB 2; Length 617;
Best Local Similarity 25.7%; Pred. No. 4.6e-24;
Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;

QY 224 KNLGTQNTLTNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAH-RNLWHIARLVLS 282
DB 183 KIVSGGHTVELPYEFLLPCLCIEASYLOEDTVRRKKCPQSWPEAYGSDFWQSIHFTDYS 242
QY 283 PG---VWQLDAPCCPLPGKVTLCWQAPDQSPQBLVPPVPQKNTVNEPQDFQVAG--H 336
DB 243 QHNQVMWALTLCPLKLEASLCWRQDPLTPCETL-----PNATAQSEGWILENVDLH 296
QY 337 PNLGVQVSTWEKVQLQA-----SWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSPG 388
DB 297 PQLCFKPFSGNSHVECPHOTGSLTSWNVSMDT-QAQLLILHFSRRYATFSAWSLPG 354
QY 389 C---TPLPSMASTRARLGEELLQD-----FRSHQCMQLNDDNMGSLWACPMKYIHR 440
DB 355 LGPDTMPFPVYSIQSGSVFVTLDIIPFLQENCLVWRSD-----VHFA 401
QY 441 WVLV-----WLACILLLAAALFFLLKKDKRKAARGSRRTALLHLSADGAGYERLVGAL 493
DB 402 WKVLCPDDAPYPTQLLL-----RSLGSGRTRPVLLHHAADSEAQRRLVGAL 448
QY 494 ASALSOM---PLRVAVDLWSRRELGAHALAWTHHRRRLQEGGVVILLFSPAAVACQ 550
DB 449 AELLRTALGGGRDVIYDLMBGTHVARIGPLPWLWAARERVAREQGTVLLLNWNCAGPS--- 505
QY 551 QWLQQLQTVFPGPHDALAAWLSVLPDLFQGRATGRVGVVFDGILLHPDSVPSPFRVAPLF 610
DB 506 -----TACSGDPOQAASLURLLCAAPRL-----LLAYFSRLCAKGDIPLRLALPRY 552
QY 611 SLPTQLPAFLDALQGGCSTSA-----GRPADRVVTVQA-----LRSALDSCSTSSSEAP 659
DB 553 RLLRLDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLEAAKDDYQGSTNSP 611

RESULT 6
US-09-747-259-16
; Sequence 16, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-747-259-16
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-773-2

Query Match
Best Local Similarity 4.6%; Score 167; DB 2; Length 864;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLIT--GPNITLN-----HTDLVPCICIQWSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGLVPLHVE-WTLQTDASILYLEGAEISVLQLNTNER 124
QY 257 --VEFCPPFRDPGAHNLWHIARLR-VLSPG-----VMQDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKP-QFLSMLQHRKRWFSHFVDPGQEVYTVHLPKP-----IPDG 171
QY 308 SPQCP----LVPPVQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDESKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KODMLLVEMKTGLNNTSV-----CA-----LEP-- 386
DB 231 Q---VLESFSDSENHSCFVVVKQIFAPROEBFHQRANVTFTLSKFHWCHHHVQVQPPF 287
QY 387 SGC-----TPLPSMASTRAARLGBELLQDFRSHQCMQWLNDDNMGSLWACPMCKY 436
DB 288 SSCNDCLRHAVTVPVINSNTVPK-----PVADY 318
QY 437 IHRWV--LVWLACLLAAALFFFL-----LLKDRRKAARG----- 472
DB 319 I-PLWVYGLITLAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHORR 529
DB 378 RPRKRWIVYSADHPLVYEVVLKFAQLITACGTEVALDLLEBQVISEVGVMTWVSQKQE 437
QY 530 ILQEGGVILLFS-----PAAVACQOQWLQLOTVBPGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKWKAILGWAEPVQLRCDHW-----KPA-GDLFTAANNMIL 490
QY 575 PDLQGRATGRYGVYFDGLLHPDSVPSPRPVAPLFSL 612
DB 491 PDPKPCFCGYVVCYFSGICSRDVPDLFNITSRYPL 528

RESULT 13
US-09-022-253-2
; Sequence 2, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694

; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-2

Query Match
Best Local Similarity 4.6%; Score 167; DB 2; Length 864;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLIT--GPNITLN-----HTDLVPCICIQWSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGLVPLHVE-WTLQTDASILYLEGAEISVLQLNTNER 124
QY 257 --VEFCPPFRDPGAHNLWHIARLR-VLSPG-----VMQDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKP-QFLSMLQHRKRWFSHFVDPGQEVYTVHLPKP-----IPDG 171
QY 308 SPQCP----LVPPVQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDESKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KODMLLVEMKTGLNNTSV-----CA-----LEP-- 386
DB 231 Q---VLESFSDSENHSCFVVVKQIFAPROEBFHQRANVTFTLSKFHWCHHHVQVQPPF 287
QY 387 SGC-----TPLPSMASTRAARLGBELLQDFRSHQCMQWLNDDNMGSLWACPMCKY 436
DB 288 SSCNDCLRHAVTVPVINSNTVPK-----PVADY 318
QY 437 IHRWV--LVWLACLLAAALFFFL-----LLKDRRKAARG----- 472
DB 319 I-PLWVYGLITLAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHORR 529
DB 378 RPRKRWIVYSADHPLVYEVVLKFAQLITACGTEVALDLLEBQVISEVGVMTWVSQKQE 437
QY 530 ILQEGGVILLFS-----PAAVACQOQWLQLOTVBPGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKWKAILGWAEPVQLRCDHW-----KPA-GDLFTAANNMIL 490
QY 575 PDLQGRATGRYGVYFDGLLHPDSVPSPRPVAPLFSL 612
DB 491 PDPKPCFCGYVVCYFSGICSRDVPDLFNITSRYPL 528

RESULT 14
US-09-022-260-2
; Sequence 2, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
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Qy	439	RRWVWLACLLAAALFFFLKKDKRKAARG-SRTALLLHSDAGAGYERLVGALAASL	497
Dd	455	LG--LLIILALLALTLLGVLTALTCRRPQSGPGPARPVLLTHAADSEAQRRLVGALAEILL	512
Qy	498	SQM---PLRVAVDVLWSRELGAHALAFPHFHORRILOEGGVVVILLFSPAAVAQCOWQLQ	554
Dd	513	RNALGGGRDIVDLMEGRHVARVGPLMNAARTVAREQGVTVLLWSGA-----D	563
Qy	555	LQTVEPGPHDALAAWLSCVLPDFLQAGRATRGVGVVFDCGLLHPDSVPSPFRVAPLSIPT	614
Dd	564	LRPVS-GPDPAAPLLA-----LLHAAFPRLLLAYFSRLCAKGDIPPLRALPRYLRLR	617
Qy	615	QLPAFLDALQG---GCSTSGAGPADPRVRVTQALRSALDSCT	653
Dd	618	DLPRLLRALDRPPAEAATSWGIGARORR-----OSRLELCSS	654

```

? sequence 326; Application US/09893/328
? Patent No. 6822082
? GENERAL INFORMATION:
? APPLICANT: Sheppard, Paul O.
? APPLICANT: Sheppard, Scott R.
? APPLICANT: Pressnell, Scott R.
? TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
? FILE REFERENCE: 00-41
? CURRENT APPLICATION NUMBER: US/09/893,737
? CURRENT FILING DATE: 2001-06-28
? PRIOR APPLICATION NUMBER: US 60/215,446
? PRIOR FILING DATE: 2000-06-30
? NUMBER OF SEQ ID NOS: 329
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 328
? LENGTH: 226
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-893-737-328

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	Query Match	8.6%	Score 310;	DB 2;	Length 667;
	Best Local Similarity	28.1%	Pred. No. 5.9e-24;		
	Matches 130;	Conservative 56;	Mismatches 214;	Indels 62;	Gaps 18
Qy	224	KNLGPNITLHNTDLVPCICIQWLSLEPDSERVEFCFPREDPGAH-RNLW----	HIARLR	279	
		:: : :: : :: : :: : :: : :: : :: :			
Dd	223	KIVSGGHTVELPYEFLLPCLCIEASYLQSDTVRRKKCPQSQWEAYGDFWKSVHFDTYS	282		
		:: : :: : :: : :: : :: : :: : :: :			
Qy	280	VLSFGVQLDAPCCLPGRVTLCKWAPDQSPCOPLVPVPVKNATVNEQDF---QLVACH	336		
		:: : :: : :: : :: : :: : :: : :: :			
Dd	283	QHTQMVALTUTRCPULKEALACQRDHMTLKCDL-----PNATARESGGVTVLSEKVDLH	336		
		:: : :: : :: : :: : :: : :: : :: :			
Qy	337	PNLCVQVSTWEKVLOA-----CSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPGSC	389		
		:: : :: : :: : :: : :: : :: : :: :			
Dd	337	PQLCFKFSFGNSSHVECPHOTGSLTSWNVMDT-OAQQLILHPSRMATSAANSLPGL	395		
		:: : :: : :: : :: : :: : :: : :: :			
Qy	390	---TPLPSMASTRARLGEEILLQD-----FRSHQCWLNDNDNMGLW---ACPMDKYTH	438		
		:: : :: : :: : :: : :: : :: : :: :			
Dd	396	GDQTLVPPVYTVSQAGSSPVSLDLIIPFLRPGCCVLVRSD-VQFAWKHLCLCPDVSYRH	454		
		:: : :: : :: : :: : :: : :: : :: :			
Qy	439	RWRVLVMWLACULLLAALPFFFLLLKKDRKKAARG-SRTALLIHSAOGAGYERLVGALASAL	497		
		:: : :: : :: : :: : :: : :: : :: :			
Dd	455	LG--LLTIALIAIMLTGLGWIALTCRRPOSGGPGPARVLLHAADSRAORRLVGALAELL	512		
		:: : :: : :: : :: : :: : :: : :: :			


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RESULT 10
US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-2

Query Match      4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY    224 KNLIT--GPNITLN-----HTDLVPCLCIQVWSLEPD-----SER 256
DB    66 KNLTPSPFKNIYINLVSSTQHGLVPVLHVE-WTLQTDSILYLEGAELSVLQLNTNER 124
QY    257 --VFPCFPREDPGAHRLNWLHIARLR-VLSFG-----VWQLDAPCCILPGKVTLCWQAPDQ 307
DB    125 LCVKF-QFLSMLQHRHRWRFRFSFHVVDFGQEYEVTVHHLPKP-----IPDG 171
QY    308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCAVOYSTWEKVOLQACSWADSLGPFF 363
DB    172 DPNHKSIIIFVDCEDSNMKMTTSCVSSGSLNDPNITVELTDQHLRVDFTLWNEST-PY 230
QY    364 KDDMLLVEMKTGLNNTSY-----CA-----LEP-- 386
DB    231 Q---VLESFSDSENHSCFDVVKQIIFAPRQBEEFHQRANVTFTLSKFHWCHHHVQVOPFF 287
QY    387 SGC-----TPLPSMASTRARALGEILLQDFRSQCMLWNDDNGSLWACPMDKY 436
DB    288 SSCLCDCLRHAVTVPFCPVISNTTYPK-----PVADY 318

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QY 437 IHRWV--LWMLACILLAAALFFFL-----LLKDRKKAARGS----- 472
DB 319 I-PLWVYGLITLIIALLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMLRVAVDLWSRRELSAHCALAWFHQR 529
DB 378 RPRKVIIVISADHPHYVEVLKFAQLITACGTEVALDLEEQVISEVGMVTWVSQRKOE 437
QY 530 ILQEGGVILLFS-----PAAVAQCOOQLQOTVBPFGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKKAILGWAEPVQLRCDHW-----KPA-GDLFTAAANNIL 490
QY 575 PDFLQGRATRGVYVFDGLLHPDSVPSPFRVAPLFSL 612
DB 491 PDFKRPACFGTVVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 11

US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-696-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;
QY 224 KNTT--GPQNTLN-----HTDLVPLCLCTQVWSLSPD-----SER 256
DB 66 KNTLPSSPKNIYINLSVSTQHGELVPVLHVE-WTLQTDASILYLEGAEISVLQNTN 124

QY 257 --VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VMOLDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKP-QFLSMLQHHRKWRFSFHFVVDPGQGEYEVTVHHLKPK-----IPDG 171
QY 308 SPCQP-----LVPVPQKNATVNEPQDFQLVAGHPNLGVQVSTWKEVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVDPDCDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KDDMLLVEMKTKLNTSV-----CA-----LEP-- 386
DB 231 Q---VLLSFSFSEHNSCFDVVVKQIFAPRQEBFHQRANVTFTLSKFHWCHHHVQVQFF 287
QY 387 SGC-----TLPSPMASTRARALGELQLDFRSHQCMQLWDDNMGSLWACPMWKY 436
DB 288 SSCINDCLRHAVTVPCPVISNTTPK-----PVADY 318
QY 437 IHRWV--LWMLACILLAAALFFFL-----LLKDRKKAARGS----- 472
DB 319 I-PLWVYGLITLIIALLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMLRVAVDLWSRRELSAHCALAWFHQR 529
DB 378 RPRKVIIVISADHPHYVEVLKFAQLITACGTEVALDLEEQVISEVGMVTWVSQRKOE 437
QY 530 ILQEGGVILLFS-----PAAVAQCOOQLQOTVBPFGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKKAILGWAEPVQLRCDHW-----KPA-GDLFTAAANNIL 490
QY 575 PDFLQGRATRGVYVFDGLLHPDSVPSPFRVAPLFSL 612
DB 491 PDFKRPACFGTVVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 12

US-08-978-773-2
; Sequence 2, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-773-2

Query Match      4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTP--GFONITLN-----HTDLVPCLCIQVWSLEPD-----SER 256
Db 66 KNLTPSPKNIYINLVSSTQHGLVPLVHYE-WTLQTDASILYLEGAELSVLQNTNER 124
QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
Db 125 LCVKFP-QFLSMLQHRRKWRFSFHFVVDPOQEYEVTVHLPKP-----IPDG 171
QY 308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQOACSWADSLGPF 363
Db 172 DPNHKSIIIFVDCEDSKMKWTTSCVSSGSLWDENITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KDDMLLVEMKTLGNNTSV-----LLKKDRRKAARGS-----LEP-- 386
Db 231 Q---VLESFSDSENHSCFVVKQIFAPROBEFHQRANVTFTLSKFHWCCHHHVQVQPF 287
QY 387 SGC-----TPLPMASTRARLGEELLQDFRSHQCMQLMNDNDNGSLWACPMCKY 436
Db 288 SSCLNDCLRHATVPCPVISNTVPK-----PAAVACQOQMLQTVBPGPHDALAAMLSCVL 574
QY 437 IHRRWV--LVWLACILLAAALFFFL-----LLKKDRRKAARGS----- 472
Db 319 I-PLWVYGLITLAILLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMPLRVAVDLWSRRELSAHGALAWFHQR 529
Db 378 RPRKVMIVYSADHPLYVEVLKFAQLITACGTEVALDLLEEQVISEVGMVTWVSROKQE 437
QY 530 ILQEGGVVILFS-----PAAVACQOQMLQTVBPGPHDALAAMLSCVL 574
Db 438 MVESNSKIIILCSRGTQAKKAILGWAEPAVOLRCDH-----KPA-GDLFTAAMNML 490
QY 575 PDFLQGRATGRYGVYFDGLLHPDSVPSPFRVAPLFSL 612
Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 13
US-09-022-253-2
; Sequence 2, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694

; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-2

Query Match      4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTP--GFONITLN-----HTDLVPCLCIQVWSLEPD-----SER 256
Db 66 KNLTPSPKNIYINLVSSTQHGLVPLVHYE-WTLQTDASILYLEGAELSVLQNTNER 124
QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
Db 125 LCVKFP-QFLSMLQHRRKWRFSFHFVVDPOQEYEVTVHLPKP-----IPDG 171
QY 308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQOACSWADSLGPF 363
Db 172 DPNHKSIIIFVDCEDSKMKWTTSCVSSGSLWDENITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KDDMLLVEMKTLGNNTSV-----LLKKDRRKAARGS-----LEP-- 386
Db 231 Q---VLESFSDSENHSCFVVKQIFAPROBEFHQRANVTFTLSKFHWCCHHHVQVQPF 287
QY 387 SGC-----TPLPMASTRARLGEELLQDFRSHQCMQLMNDNDNGSLWACPMCKY 436
Db 288 SSCLNDCLRHATVPCPVISNTVPK-----PAAVACQOQMLQTVBPGPHDALAAMLSCVL 574
QY 437 IHRRWV--LVWLACILLAAALFFFL-----LLKKDRRKAARGS----- 472
Db 319 I-PLWVYGLITLAILLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMPLRVAVDLWSRRELSAHGALAWFHQR 529
Db 378 RPRKVMIVYSADHPLYVEVLKFAQLITACGTEVALDLLEEQVISEVGMVTWVSROKQE 437
QY 530 ILQEGGVVILFS-----PAAVACQOQMLQTVBPGPHDALAAMLSCVL 574
Db 438 MVESNSKIIILCSRGTQAKKAILGWAEPAVOLRCDH-----KPA-GDLFTAAMNML 490
QY 575 PDFLQGRATGRYGVYFDGLLHPDSVPSPFRVAPLFSL 612
Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 14
US-09-022-260-2
; Sequence 2, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-260-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTT--GPQNTLTL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSMQLQHRRKWRPFSFHFVDPQGEYEVTVHHLPKP-----IPDG 171

QY 308 SPQCP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCESKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230

QY 364 KDDMLLVEMTKTGLNNTSV-----CA-----LSP-- 386
DB 231 Q-----VLLSEFSDSENHSCFDVVVKQIFAPROBEFHQRANVTTLTKFHWCHHHVQVQFPF 287

QY 387 SGC-----TPLFSMASTRARLGEELLQDFRSHQCQWLWDDNMGSLMACPMCKY 436
DB 288 SSCNLDCRLRAVTVPCPVISNTTPK-----PVADY 318

QY 437 IHRRW--LWVLAALLAALFPFL-----LLKORRKAARGS----- 472
DB 319 I-PLWVYGLTILAILLVGVSIVLIIQWTLRSLGADQKGGDDSKINGILPVADLTTPPL 377

QY 473 --RTALLHSGADGVERLYGALASAL--SQMPLRVAVDLMSRRRLSAHGALEWHFHQRRR 529
DB 378 RPRKRWIVISADHPLYVEVVLKFAQLITACGTEVALDLLEEQVISEVGVMTWVSROKQE 437

QY 530 ILQEGGVVILLFS-----PAAVAQCQQLQLTQVPEPGFHDAALAWLSCVL 574

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-259-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTT--GPQNTLTL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSMQLQHRRKWRPFSFHFVDPQGEYEVTVHHLPKP-----IPDG 171

QY 308 SPQCP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCESKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-259-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTT--GPQNTLTL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSMQLQHRRKWRPFSFHFVDPQGEYEVTVHHLPKP-----IPDG 171

QY 308 SPQCP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCESKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
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Qy 364 KDDMLLVEMKTLNNTSV-----CA-----LEP-- 386
Db 231 Q---VLESFSDSENHSCFDVVKQIFAPROEFHORANVTFTLSKFHWCCHHVQVQFFF 287
Qy 387 SGC-----TPLPSMASTRARLGEELLODFRSHQCQQLWDDNMGSLWACPMCKY 436
Db 288 SSCLNDCLRHAVTVCPCVISNTTVPK-----PVADY 318
Qy 437 IHRWV--LVWLACLLAAALFFFL-----LLKDRRKAARG- 472
Db 319 I-PLWVYGLITLIALIVGSIIVLIICTWRLSGADQEKHGDDSKINGILFVADLTTPPL 377
Qy 473 --RTALLHSADGAGYERLVCALASAL--SQMPLRVAVDLWSRRELSAHGALAWFHQRRR 529
Db 378 RPRKVMIVISADHPLYVEWVLKFAQLITACGTEVALDLLLEEQVISEVGVNMTWVSROKQE 437
Qy 530 ILQEGGVVILLFS-----PAAVACCOOWLQQTVEPQPHDALAAWLSCVL 574
Db 438 MVESNSKIIILCSRGTOAKWKAILGWAEPVQLRCDHW-----KPA-GDLFTAAMNML 490
Qy 575 PDFLQGRATGRYGVYFDGLLHPDSVSPFRVAFLESL 612
Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
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Search completed: August 16, 2006, 11:47:54
Job time : 55 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:48:07 ; Search time 35 Seconds
(without alignments)
1304.753 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSFWLLSLALGRNPVVVS.....SSEAPGCCSEWDLGCTTLE 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2339	64.9	705	6	US-10-196-749-598
2	2339	64.9	705	7	US-11-311-555-14
3	2339	64.9	705	7	US-11-311-561-14
4	2339	64.9	705	7	US-11-101-316-162
5	2339	64.9	705	7	US-11-311-554-14
6	2339	64.9	705	7	US-11-376-673-162
7	1086	30.1	343	7	US-11-293-697-2756
8	739	20.5	261	7	US-11-293-697-3960
9	338.5	9.4	637	7	US-11-253-200-14
10	337.5	9.4	661	7	US-11-253-200-111
11	313.5	8.7	609	7	US-11-253-200-8
12	310	8.6	589	7	US-11-253-200-5
13	310	8.6	627	7	US-11-253-200-21
14	310	8.6	650	7	US-11-253-200-107
15	310	8.6	667	7	US-11-311-555-16
16	310	8.6	667	7	US-11-311-561-16
17	310	8.6	667	7	US-11-311-554-16
18	310	8.6	667	7	US-11-253-200-2
19	309	8.6	551	7	US-11-293-697-3946
20	282.5	7.8	591	7	US-11-253-200-161
21	167	4.6	864	7	US-11-312-797-2
22	166	4.6	279	7	US-11-253-200-121
23	166	4.6	391	7	US-11-253-200-15
24	151.5	4.2	866	7	US-11-312-797-4
25	137.5	3.8	534	7	US-11-253-200-124

Sequence 9, Appli
Sequence 113, App
Sequence 6, Appli
Sequence 122, App
Sequence 3, Appli
Sequence 109, App
Sequence 92, Appli
Sequence 84, Appli
Sequence 100, App
Sequence 12, Appli
Sequence 11, Appli
Sequence 3942, Ap
Sequence 23, Appli
Sequence 5161, Ap
Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 772, App
Sequence 2959, Ap

26 137 3.8 373 7 US-11-253-200-9
27 133.5 3.7 279 7 US-11-253-200-113
28 133.5 3.7 376 7 US-11-253-200-6
29 133.5 3.7 414 7 US-11-253-200-122
30 133.5 3.7 454 7 US-11-253-200-3
31 131.5 3.6 414 7 US-11-253-200-109
32 128.5 3.6 351 7 US-11-253-200-92
33 128.5 3.6 429 7 US-11-253-200-84
34 128.5 3.6 636 7 US-11-253-200-102
35 128.5 3.6 714 7 US-11-253-200-100
36 122.5 3.4 510 7 US-11-253-200-12
37 122.5 3.4 533 7 US-11-253-200-11
38 121 3.4 390 7 US-11-293-697-3942
39 117 3.2 421 7 US-11-253-200-23
40 110.5 3.1 3575 7 US-11-330-403-5161
41 104.5 2.9 1237 7 US-11-045-540-4
42 104.5 2.9 1248 7 US-11-045-540-5
43 104 2.9 964 6 US-10-142-275B-2
44 102.5 2.8 3020 7 US-11-140-487A-772
45 98.5 2.7 354 7 US-11-293-697-2959

ALIGNMENTS

RESULT 1

US-10-196-749-598

; Sequence 598, Application US/10196749

; Publication No. US20060094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Zhang, Zemin

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC340

; CURRENT APPLICATION NUMBER: US/10/196,749

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 598

; LENGTH: 705

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-196-749-598

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Query Match      64.9%; Score 2339; DB 6; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

QY 1 MPVSWFLSLALGRNPVVVLSERLMEPDTCARCSLGLSCHLWDGVLCLPGSLQAPGV 60
Db 1 MPVWFLSLALGRSPVVLSERLVGPQDATHCSPLSCRLWSDILCLPGDIVPAPGV 60
QY 61 LVPTLQTELVLRCQKTDCCALRVVVVHLAVHGWAEPEE-----AGKSDSELOERNAS 116
Db 61 LAPTHLQTELVLRCQKTDCCALRVVHLAVHGWAEPEE-----AGKSDSELOERNAS 120
QY 117 LQAVVLSFQAYPTARCALEVVQVPAALVQVQSGVSAVDFCFEASIGAEVQIWSYTKPR 176
Db 121 LQAVVLSFQAYPTARCVLLEVVQVPAALVQVQSGVSVVYDCFEAALGSEVRINWSTQPR 180
QY 177 YQKELNLTQQLP-----DGDVLLTLTVSEEQDFSFLLYLPRVPPDALKSLWYKNLT 227
Db 181 YKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFLGLSLYMNQVQPPKPRWHKNLT 240
QY 228 GPQNTLNTHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSGVWQ 287
Db 241 GPQIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHQNLWQAARLLTLQSWL 300
QY 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNAIVNEPQDFOLVAGHPNLCVQVSTWE 347
Db 301 LDAPCSLPAEALCWRAPEGDPGCPQLVPPPLSWENVTVDKVLFPPLKHPNLCVQVNSSE 360
QY 348 KVQLQACSWADSLGPFKDDMLIVEMKTGLNNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KLQLECLWADSLGFLKDDVLLLETRGPQDNRLSCALPESGCTSLPSKASTRAARLGEYL 420
QY 408 LQDFRSHOCMLWDDNMGSLWACPMCKYIHRRWVWLWACLILLAAALFFFLKDKRRK 467
Db 421 LQDLQSGQCQLQW-DDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKOHAK 479
QY 468 -----AAGSRRTALLHSADGAGYERLVGALASALSQMPURVAVDLWSRRE 513
Db 468 -----AAGSRRTALLHSADGAGYERLVGALASALSQMPURVAVDLWSRRE 513

Query Match      64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

QY 1 MPVSWFLSLALGRNPVVVLSERLMEPDTCARCSLGLSCHLWDGVLCLPGSLQAPGV 60
Db 1 MPVWFLSLALGRSPVVLSERLVGPQDATHCSPLSCRLWSDILCLPGDIVPAPGV 60
QY 61 LVPTLQTELVLRCQKTDCCALRVVVVHLAVHGWAEPEE-----AGKSDSELOERNAS 116
Db 61 LAPTHLQTELVLRCQKTDCCALRVVHLAVHGWAEPEE-----AGKSDSELOERNAS 120
QY 117 LQAVVLSFQAYPTARCALEVVQVPAALVQVQSGVSAVDFCFEASIGAEVQIWSYTKPR 176
Db 121 LQAVVLSFQAYPTARCVLLEVVQVPAALVQVQSGVSVVYDCFEAALGSEVRINWSTQPR 180
QY 177 YQKELNLTQQLP-----DGDVLLTLTVSEEQDFSFLLYLPRVPPDALKSLWYKNLT 227
Db 181 YKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFLGLSLYMNQVQPPKPRWHKNLT 240
QY 228 GPQNTLNTHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSGVWQ 287
Db 241 GPQIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHQNLWQAARLLTLQSWL 300
QY 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNAIVNEPQDFOLVAGHPNLCVQVSTWE 347
Db 301 LDAPCSLPAEALCWRAPEGDPGCPQLVPPPLSWENVTVDKVLFPPLKHPNLCVQVNSSE 360
QY 348 KVQLQACSWADSLGPFKDDMLIVEMKTGLNNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KLQLECLWADSLGFLKDDVLLLETRGPQDNRLSCALPESGCTSLPSKASTRAARLGEYL 420
QY 408 LQDFRSHOCMLWDDNMGSLWACPMCKYIHRRWVWLWACLILLAAALFFFLKDKRRK 467
Db 421 LQDLQSGQCQLQW-DDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKOHAK 479
QY 468 -----AAGSRRTALLHSADGAGYERLVGALASALSQMPURVAVDLWSRRE 513
Db 468 -----AAGSRRTALLHSADGAGYERLVGALASALSQMPURVAVDLWSRRE 513

US-11-311-555-14
GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
```

Db 480 GWRLKQDVRSAAARG-RAALLYSADDSGFERLVGALASALCOLPVRVAVDLWSRRE 538
Qy 514 LSAHGALAFHQRRIILQEGGWILLSPAAVACQOWLOQTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQRRTLOEGGVVLLSPGVALCSEWLQDGVSGPGAHGPHDAFRASL 598
Qy 571 SCVLPDFLOQRATGRVYVFDGLIHPDSVSPRVAFLPSIPTQLPAFLDALQGCST 630
Db 599 SCVLPDFLOQRAPSGVYVACFDRLLHPDAVPAFLFTVFTPLPSQLPDFLQALQOPR 658
Qy 631 AGRPADRVERTQALRSALDSC--TSSSEAPG 660
Db 659 SGRQERAEQVSRALQPALDSYFHPGTPAG 690

RESULT 3

US-11-311-561-14
; Sequence 14, Application US/11311561
; Publication No. US2006008917A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 US/11/311,561
; CURRENT APPLICATION NUMBER: US/11/311,561
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39

SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-311-561-14

Query Match 64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

Qy 1 MPVSVFLSLAIGRPVVPVLSRLMBPQDTRARCSLGLSCHLWDGVLCLPGSLQSPGPV 60
Db 1 MPVSVFLSLAIGRPVVPVLSRLMBPQDTRARCSLGLSCHLWDGVLCLPGSLQSPGPV 60
Qy 61 LVPTRLQTLVLRCKQKTDCLARVVRVVLAVHGHABPEE-----AGKSSESELOESNAS 116
Db 61 LAPTHLQTLVLRCKQKTDCLARVVRVVLAVHGHABPEE-----AGKSSESELOESNAS 120
Qy 117 LQAQVVLSPQAPYPIARCALLEVQVPADLVQPGSVGSNAFDCFEASIGARVQIWSYTKPR 176
Db 121 LQAQVVLSPQAPYPIARCALLEVQVPADLVQPGSVGSNAFDCFEASIGARVQIWSYTKPR 180
Qy 177 YQKELNLTQOLP-----DGDVNLTLTVSEEQDFSLLYLRVPVDPALKSLWYKNLT 227
Db 181 YQKELNLTQOLP-----DGDVNLTLTVSEEQDFSLLYLRVPVDPALKSLWYKNLT 240
Qy 228 GPQNTLNHTDLVPCLCIQVMSLEPDSERVECPFPREDPCAHRNLWHIARLRLVSPGVWQ 287
Db 241 GPQNTLNHTDLVPCLCIQVMSLEPDSERVECPFPREDPCAHRNLWHIARLRLVSPGVWQ 300
Qy 288 LDAPCCLPGKVTLCWOAPDQSPQPLVPPVPOKNAVNEPQDFQLVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPGKVTLCWOAPDQSPQPLVPPVPOKNAVNEPQDFQLVAGHPNLCVQVSTWE 360
Qy 348 KYQLQACSWADSLGPFKDDMLVEMKTLNNTSVCALEPSGCTPLPSMASTRARLGEEL 407
Db 361 KYQLQACSWADSLGPFKDDMLVEMKTLNNTSVCALEPSGCTPLPSMASTRARLGEEL 420
Qy 408 LQDFRSHOCMLWDDNMGSLWACPMCKYIHRRWLVWLACLLAAALPFLLLKKDRRK 467
Db 421 LQDFRSHOCMLWDDNMGSLWACPMCKYIHRRWLVWLACLLAAALPFLLLKKDRRK 479
Qy 468 -----AARGSRRTALLHSADGAGVRLVGLASALSQMPLRVAVDLWSRRE 513
Db 480 GWRLKQDVRSAAARG-RAALLYSADDSGFERLVGALASALCOLPVRVAVDLWSRRE 538
Qy 514 LSAHGALAFHQRRIILQEGGWILLSPAAVACQOWLOQTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQRRTLOEGGVVLLSPGVALCSEWLQDGVSGPGAHGPHDAFRASL 598
Qy 571 SCVLPDFLOQRATGRVYVFDGLIHPDSVSPRVAFLPSIPTQLPAFLDALQGCST 630
Db 599 SCVLPDFLOQRAPSGVYVACFDRLLHPDAVPAFLFTVFTPLPSQLPDFLQALQOPR 658
Qy 631 AGRPADRVERTQALRSALDSC--TSSSEAPG 660
Db 659 SGRQERAEQVSRALQPALDSYFHPGTPAG 690

RESULT 4

US-11-101-316-162
; Sequence 162, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252


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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-162

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Query Match	64.9%;	Score 2339;	DB 7;	Length 705;
Best Local Similarity	66.3%;	Pred. No. 4.7e-198;		
Matches 459;	Conservative	66;	Mismatches 133;	Indels 34;
Gaps	7;			
Qy	1	MPVSWFLLSALGNPPVVSILERLMEQDTCARCSIGLSCHLWDGDLVCLPGSLQSAQGPV	60	
Db	1	MPVWFLLSLALGKSPVLSLRLVUGQDATHCSFGLSCRWDSDILCPGDIVPAPGPV	60	
Qy	61	LVPTRLQTELVLRCPOKTCALRVVRVVVHLAVHGHWAEPSE---	AGKSDSELOESRNAS	116
Db	61	LAPTHQLTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPNRS	120	
Qy	117	LQOQVLSFOAYPTARCALLLEVQVPADLVQPGQSVGSVAFCFPAASLGAQVQIWSYTKPR	176	
Db	121	LQOQVLSFOAYPTARCVLLEVQVPAAVLQPGQSVGVVYDCFFAALGSEVRVWSYTOPR	180	
Qy	177	YQKELNLTQQLP-----DGNVLLTLVDVSEQDPSFTLLYLRPVPDALKSLWYKNLT	227	
Db	181	YKELNHTQQLPALPWLNVSGADGNVHLVNVSEQHFGLSLYWNQVQPPKPRHKNLT	240	
Qy	228	GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCFPREDPGAHRLNMLHILARLVLSPGVMQ	287	
Db	241	GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICFPREDPRAHQLNMQAARLLTLQSWL	300	
Qy	288	LDAPCCLPGKVTLICQWAPDQSPCQPLVPPVPQKNATVNEPDQFQVLVAGHPNLCVQVSTWE	347	
Db	301	LDAPCSLPAAEALCWRAPGGPGCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSE	360	
Qy	348	KVQLQACSWADSLGPFDDMLLVEMTKLNNTSVCALEPSCCTPLPSMASTAAARLGEEL	407	
Db	361	KLQLECLWADSLGFLDVLLETRGPDNRSLCALEPSCCTSLPSKASTAARLGBYL	420	
Qy	408	LQDPRSHQCMLWMDNNGSLWACPMDKYIHRRWVLVWLACLLAAALFFFLLLKKDRKK	467	
Db	421	LQDLQSGCQLWL-DDDLGALWACPMDKYIHKRWALVWLACLLFAAALSILLKKDHAK	479	
Qy	468	-----AAGRSRTALLHSGADGAGYERLVGALASALSQMPLRVAVDLWSRRE	513	
Db	480	GWLRLLLKQDVRSGAAARG-RAALLLYSADDGSGFERLVGALASALCQLPLRVAVDLWSRRE	538	
Qy	514	LSAHGALAWFHQRRRLIOEGGVVILLFSPAAVAQCQOWILOQVTEP---	GPHDALAAML	570
Db	539	LSAQGPVAMFHAQRQRTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHPHDAFRASL	598	
Qy	571	SCVLPDFLQGRATRGYGVVFDGLLHPDSVPSPRVAPFLSPTQLPAFLDALOGGCGTS	630	
Db	599	SCVLPDFLQGRAPGSYVGACEDRLHPDAVPAFLFTVPVFTLPSQLPDFLQALQOPAPR	658	
Qy	631	AGRPADRVERTQALRSALDSC--TSSEAPG	660	
Db	659	SGRLQREAEQVSRALQALPSYFHPGTPAGP	690	

RESULT 5
US-11-311-554-14
; Sequence 14, Application US/11311554
; Publication No. US20060134755A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey

```

: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Li, Hanzhong
: APPLICANT: Hillan, Kenneth
: APPLICANT: Tumas, Daniel
: APPLICANT: VanLookeren, Menno
: APPLICANT: Vandlen, Richard
: APPLICANT: Watanabe, Colin
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William
: APPLICANT: Yansura, Daniel
: TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
: FILE REFERENCE: P1381R1C1P1(US)
: CURRENT APPLICATION NUMBER: US/11/311,554
: CURRENT FILING DATE: 2005-12-20
: PRIOR APPLICATION NUMBER: US/09/747,259
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: US 09/311,832
: PRIOR FILING DATE: 1999-05-14
: PRIOR APPLICATION NUMBER: US 60/172,096
: PRIOR FILING DATE: 1999-12-23
: PRIOR APPLICATION NUMBER: PCT/US99/31274
: PRIOR FILING DATE: 1999-12-30
: PRIOR APPLICATION NUMBER: US 60/175,481
: PRIOR FILING DATE: 2000-01-11
: PRIOR APPLICATION NUMBER: PCT/US00/04341
: PRIOR FILING DATE: 2000-02-18
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 60/191,007
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: PCT/US00/07532
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: PCT/US00/15264
: PRIOR FILING DATE: 2000-06-02
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 39
: SEQ ID NO 14
: LENGTH: 705
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-11-311-554-14

```

[illegible]

RESULT 5
US-11-311-554-14
; Sequence 14, Application US/11311554
; Publication No. US20060134755A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey

Db 361 KQLOECLWADSLGKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
Qy 408 LQDFRSHQCHQWLDNDNGSLWACPMCKYIHRVWLVWLCALLAAALFFFLLLKKORRK 467
Db 421 LQDQSGOCLQW-DDDLGALWACPMCKYIHKRWLVWLCALLFAAALLSLLLKKOHAK 479
Qy 468 -----AAGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRE 513
Db 480 GWRLLKQDVRSGAAARG-RAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRE 538
Qy 514 LSAHGALEWFFHQRRILOEGGVVLLFSPAAVAQCOOVLQOTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQAQRRTLOEGGVVLLFSPGAVALLCSEWLDQGVSGGAGHGFHDAFRASL 598
Qy 571 SCVLPDFLOGRATGRYVGVYFDGLLHPSVSPFRVAPLFLSLTQLPALFDALQGCST 630
Db 599 SCVLPDFLOGRAPGSYVGACFDRLHDPDAVPALEFVFTLPSQDFLQALQOPRPR 658
Qy 631 AGRPADRVVTVQALRSALDSC--TSSSEAPG 660
Db 659 SGRLOERAEQVSRALQALDLSYFHPGTPAPG 690

RESULT 6
US-11-376-673-162
; Sequence 162, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; TITLE OF INVENTION: LUNG TUMOR
; FILE REFERENCE: P3230R1C165C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-376-673-162

Query Match 64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

Qy 1 MPVSWFLLSALGHNPPVVSILRLWEPQDTCARCSLGLSCHLWDGDLVCLPGSLQSAQPV 60
Db 1 MPVFWFLLSALGHSPPVLSLRLVUGPDATHCSPLGSLRWDSDILCLPGDIPVAPGV 60
Qy 61 LVPTLQTLVLRCPQKTDCAALRVVVVHLAVHGHWAEPB-----AGKSDSELOESRNAS 116
Db 61 LAPTHLQTLVLRCKQETDCDLCLURVAVHLAVHGHWEPEDEEKFGGAADSGVBEPRNAS 120
Qy 117 LQAVQLSFOAYPTARCALLEVQPADLVQPGQSGSAVFDFCFEASLCAEYQIWSYTKPR 176
Db 121 LQAVQLSFOAYPTARCALLEVQPADLVQPGQSGSVVYVDFCFEALGSEVRIWSYTOPR 180
Qy 177 YOKELNLTQLP-----DGDNVLTLTDSVEQDPFSLLYLRPVPDALKSLWYKNLT 227
Db 181 YOKELNLTQLPALPWLNVSDAGDNVHLVNLVNSEQHFGLSLYWNQVQGPFPKPRHKNLT 240

Qy 228 GPQNTILNHTDLVPLCLCIQVMSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSPGVQ 287
Db 241 GPQIITLNTDLVPLCLCIQVWLEPDSVRTNICPPREDPRAHQNLWQAARLRLTLQSWL 300
Qy 288 LDAPCCLPGKVTLCQWAPDQSPCQPLVPPVPKOKNATVNPQDFQPLVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPAEALCWRAPGDPCQPLVPPPLSWENVTVDKVLBPPLLKHPNLCVQVNSSE 360
Qy 348 KVQLOACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMASTRAARLGEEL 407
Db 361 KLOQCECLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
Qy 408 LQDFRSHQCHQWLDNDNGSLWACPMCKYIHRVWLVWLCALLAAALFFFLLLKKORRK 467
Db 421 LQDQSGOCLQW-DDDLGALWACPMCKYIHKRWLVWLCALLFAAALLSLLLKKOHAK 479
Qy 468 -----AAGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRE 513
Db 480 GWRLLKQDVRSGAAARG-RAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRE 538
Qy 514 LSAHGALEWFFHQRRILOEGGVVLLFSPAAVAQCOOVLQOTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQAQRRTLOEGGVVLLFSPGAVALLCSEWLDQGVSGGAGHGFHDAFRASL 598
Qy 571 SCVLPDFLOGRATGRYVGVYFDGLLHPSVSPFRVAPLFLSLTQLPALFDALQGCST 630
Db 599 SCVLPDFLOGRAPGSYVGACFDRLHDPDAVPALEFVFTLPSQDFLQALQOPRPR 658
Qy 631 AGRPADRVVTVQALRSALDSC--TSSSEAPG 660
Db 659 SGRLOERAEQVSRALQALDLSYFHPGTPAPG 690

RESULT 7
US-11-293-697-2756
; Sequence 2756, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2756
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2756

Query Match 30.1%; Score 1086; DB 7; Length 343;
Best Local Similarity 67.0%; Pred. No. 7.4e-88;
Matches 217; Conservative 35; Mismatches 66; Indels 6; Gaps 3;

Qy 342 QVSTWKEVQLOACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMASTRAA 401
Db 6 QVNSSEKLOQCECLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAA 65
Qy 402 RLGEELLQDFRSHQCHQWLDNDNGSLWACPMCKYIHRVWLVWLCALLAAALFFFLLL 461
Db 66 RLGEVLLQDLSGQCLQW-DDDLGALWACPMCKYIHKRWLVWLCALLFAAALLSLLL 124
Qy 462 KDKRRAAARGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSSAHGALA 521
Db 125 KDKHKAARAARGAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSSAQGPVA 184
Qy 522 WFHQRRILOEGGVVILLFSPAAVAQCOOVLQOTVEP---GPHDALAAWLSCVLPDFL 578
Db 185 WFHAQRRTLOEGGVVILLFSPCAVALCSEWLDQGVSGGAGHGFHDAFRASLSCVLPDFL 244

QY 579 QGRATGVYGVYFDGLHPDSVPFPRVAPLFSIPTQLPAFLDALOGGCSSTAGPADRV 638
Db 245 QGRAPGSVVGACFDRLLHDPADVPALFRTVFTLPSQLPDLFGALQOPRAPRSGRLOERA 304
QY 639 ERVTQALRSALDSC--TSSSEAPG 660
Db 305 EQVSEALQPALDSYFHPGCTPAPG 328

RESULT 8

US-11-293-697-3960
; Sequence 3960, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3960
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3960

Query Match 20.5%; Score 739; DB 7; Length 261;
Best Local Similarity 63.2%; Pred. No. 2.2e-57;
Matches 156; Conservative 22; Mismatches 49; Indels 20; Gaps 4;

QY 433 MDKVIHRWLVWLACLLAAALFFLLKKDRK-----AARGSRATLL 478
Db 1 MDKVIHRWLVWLACLLFAAALLILLKKDHAKGWLRLKQDVRSAAAARG-RAALL 59
QY 479 HSADGAGVERLVGALASALSMPLRVAVDLWSRRELSAHGALWPHHQRRILOEGGVI 538
Db 60 YSADDSGFERLVGALAGALCQLPLRVAVDLWSRRELSAQGPVAFHQAQRRTLOEGGVV 119
QY 539 LFSPPAAVQAOQWLQOTVEP---GHDALAAMLSCLVLPDLOGRATGVYGVYFDGL 595
Db 120 LFSPPGAVLSEWLDQGVSGFGAHGPHDAFRLSCLVLPDLOGRATGVYGVYFDGL 179
QY 596 HPDSVPFPRVAPLFSIPTQLPAFLDALOGGCSSTAGPADRVVTOALRSALDSC--T 653
Db 180 HPDAVPALFRTVFTLPSQLPDLFGALQOPRAPRSGRLOERAQVSEALQPALDSYFHP 239
QY 654 SSSSEAPG 660
Db 240 PGTPAPG 246

RESULT 9

US-11-253-200-14
; Sequence 14, Application US/11253200
; Publication No. US20060142192A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Appleby, Mark W.
; APPLICANT: Lewis, Katherine E.
; APPLICANT: McKernan, Patricia A.
; APPLICANT: Okada, Shannon L.
; APPLICANT: Taft, David W.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Levin, Steven D.
; TITLE OF INVENTION: SOLUBLE ZCYTOR21, ANTI-ZCYTOR21
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION

; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 60/619,651
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/622,207
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-200-14

Query Match 9.4%; Score 338.5; DB 7; Length 637;

Best Local Similarity 27.5%; Pred. No. 1.8e-21;
Matches 131; Conservative 56; Mismatches 22; Indels 67; Gaps 18;

QY 224 KNLTPQNTITLHNTDLVPCLCIQWWSLEPDSERVFCEPREDPGAH-RNLWHIARLRVLS 282
Db 183 KIVSGGHTVDLPYEFLLPCMCIEASYLOEDTVRRKKCPQSWPEAYGDFWQSIREFTDS 242
QY 283 PG---VMOLDAPCCLPKGVTLWCQAPDOSPCOPLVPPVPQKNATVNEPODFOLVAG---H 336
Db 243 QHNQVMALTLCPLKLEASLCWRQDPLTPCETL-----PNATAQSESGWILENVDLH 296
QY 337 PNLGVQSVTWEKVQLQAC-----SWADSLGPPFKDDMLLVEMKTLGLNNTSVCALEPSG 388
Db 297 PQLCFKFS-FENSSHVECPHQSGSLPSTVSMDT-QAQLTLHFSSRTVATFSAAWSDPG 354
QY 389 C---TPLPMSMASTRARLGEELLQD-----FRSHOCMLNDDNMGSLW---ACPMDKYI 437
Db 355 LGPDTMPMPVYSISQTGQSVFVTLIIIPFLQENCILVWRSRSD-VHFAWKHVLCP--DVS 411
QY 438 HRRWLVWLACLLAAALFFLLKKDRKKAARG-SRTALLHSAAGAGYERLVGALASA 496
Db 412 HRHGLLTLALALATLVGVVVLVLLGRLLPGSGRTRPVLLHHAADSEARQLVGLALAE 471
QY 497 LSQM---PLRVAVDLWSRRELSAHGALWPHHQRRILOEGGVIILFSPAAVQAOQWL 553
Db 472 LRTALGGGRDVIDLWEGTHVARIGFLPWLMAARERVARERQGTVLLLWNCAGFS----- 525
QY 554 QLQTVPECPHDAALAWLSCLVLPDLOGRATGVYGVYFDGLHPDSVPFPRVAPLFSLP 613
Db 526 --TACSGDPQAASRLTLCAAPRPL-----LLAYFSRLCAKGDIPRLPLPRYRL 575
QY 614 TQLPAFLDALOGGCSSTA-----GRPADRVVTOA---LRSALDSCSSSEAP 659
Db 576 RDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLELEAAKDDYQGSTNSP 631

RESULT 10

US-11-253-200-111
; Sequence 111, Application US/11253200
; Publication No. US20060142192A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Appleby, Mark W.
; APPLICANT: Lewis, Katherine E.
; APPLICANT: McKernan, Patricia A.
; APPLICANT: Okada, Shannon L.
; APPLICANT: Taft, David W.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Levin, Steven D.
; TITLE OF INVENTION: SOLUBLE ZCYTOR21, ANTI-ZCYTOR21
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18

us-10-719-202-2.rapbn

Tue Aug 22 11:34:38 2006

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; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/11/311,555
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-311-555-16

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Query Match 8.6%; Score 310; DB 7; Length 667;
Best Local Similarity 28.1%; Pred. No. 6.3e-19;
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

QY 224 KNLGTPQNTLHNTDLPCLCIQVMSLEPDSERVFCEPREDPCGAH-RNLW---HIARLR 279
DB 223 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 282
QY 280 VLSPGVQWLDAPCCIPGKVTLCWQAPDQSPQPLVPPVPOKNAVNEPQDF---QLVAGH 336
DB 283 QHTQVMWALTLCPLKLEAALCORHWHTLCKDL-----PNATARESDGWVLEKVDLH 336
QY 337 PNLGVQVSTWVKVQLQA-----CSWADSLGPFKDDMLLVEMKTLNNTSVCALEPSGC 389
DB 337 POLCFKFSFGNSHVECHPQTSGLTSWNVSMDT-QAQQILHFFSRMHATFSAAWSLPGL 395
QY 390 ---TLPFSMASTRAARLGEELLQD-----FRSHQCHQMLWDDNMGSLW---ACPMKDYIH 438
DB 396 GQDTLVPPVTVSQARGSSPVSLDLIIPFLRPGCCVWVRSD-VQFAMKHLCPDVSYPH 454
QY 439 RRWLVWLAACLLAAALPFFLLKKDRKAARG-SRTALLHLSADGAGYERLVGALASAL 497
DB 455 LG--LLILALLALTLLGVVLTCTRRPQSGFPGPARPVLLHHAADSEARQLVGALELL 512
QY 498 SOM---PLRVAVDLWSRRELSSAHGALAWFHQRRIILQEGGVVILLFSPAQAQCOQWLQ 554
DB 513 RAALGGGRDVIWDLMEGRHVARVGPLWMAARTVAREQGTVLLWSGA-----D 563
QY 555 LQTVPEPQPHDALAAWLSVLPDFLQGRATGRYGVYFDGLLHSDPSVSPFRVAPLPSLPT 614
DB 564 LRPVS-GPDPRAPPLA-----LHAAPRPLLILAYSRCLCAKGDIPPLRALPRYELLR 617
QY 615 QLPAPFLDALQ---GCSTSAGRPAADRVERTVQALRSALDSCT 653
DB 618 DLPRLLRALDARPPAATSWGRIGARQRR-----QSRLELCS 654

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Search completed: August 16, 2006, 11:51:40
Job time : 36 secs

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; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 60/619,651
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/622,207
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-253-200-107

Query Match 8.6%; Score 310; DB 7; Length 650;
Best Local Similarity 28.1%; Pred. No. 6.1e-19;
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

QY 224 KNLGTPQNTLHNTDLPCLCIQVMSLEPDSERVFCEPREDPCGAH-RNLW---HIARLR 279
DB 206 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 265
QY 280 VLSPGVQWLDAPCCIPGKVTLCWQAPDQSPQPLVPPVPOKNAVNEPQDF---QLVAGH 336
DB 266 QHTQVMWALTLCPLKLEAALCORHWHTLCKDL-----PNATARESDGWVLEKVDLH 319
QY 337 PNLGVQVSTWVKVQLQA-----CSWADSLGPFKDDMLLVEMKTLNNTSVCALEPSGC 389
DB 320 POLCFKFSFGNSHVECHPQTSGLTSWNVSMDT-QAQQILHFFSRMHATFSAAWSLPGL 378
QY 390 ---TLPFSMASTRAARLGEELLQD-----FRSHQCHQMLWDDNMGSLW---ACPMKDYIH 438
DB 379 GQDTLVPPVTVSQARGSSPVSLDLIIPFLRPGCCVWVRSD-VQFAMKHLCPDVSYPH 437
QY 439 RRWLVWLAACLLAAALPFFLLKKDRKAARG-SRTALLHLSADGAGYERLVGALASAL 497
DB 438 LG--LLILALLALTLLGVVLTCTRRPQSGFPGPARPVLLHHAADSEARQLVGALELL 495
QY 498 SOM---PLRVAVDLWSRRELSSAHGALAWFHQRRIILQEGGVVILLFSPAQAQCOQWLQ 554
DB 496 RAALGGGRDVIWDLMEGRHVARVGPLWMAARTVAREQGTVLLWSGA-----D 546
QY 555 LQTVPEPQPHDALAAWLSVLPDFLQGRATGRYGVYFDGLLHSDPSVSPFRVAPLPSLPT 614
DB 547 LRPVS-GPDPRAPPLA-----LHAAPRPLLILAYSRCLCAKGDIPPLRALPRYELLR 600
QY 615 QLPAPFLDALQ---GCSTSAGRPAADRVERTVQALRSALDSCT 653
DB 601 DLPRLLRALDARPPAATSWGRIGARQRR-----QSRLELCS 637

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RESULT 15

US-11-311-555-16
Sequence 16, Application US/11311555
Publication No. US20060088916A1

```

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P Mickey

```
